

OM nucleic - nucleic search, using sw model

Run on: July 7, 2004, 10:48:26 ; Search time 6758 Seconds  
(without alignments)  
12160.509 Million cell updates/sec

Title: US-10-624-932-1  
Perfect score: 2752  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
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4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*

28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Query					Description
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	2	950.4	34.5	2791	29	AY406493 Mus muscu
	3	923.4	33.6	3790	11	AK031655 Mus muscu
	4	872.4	31.7	3866	11	AK018177 Mus muscu
	5	814	29.6	2802	29	AY406492 Pan trogl
	6	810.4	29.4	2532	29	AY411747 Homo sapi
	7	780.4	28.4	2532	29	AY411749 Mus muscu
	8	768.6	27.9	1034	12	BI758231 603029876
	9	736.6	26.8	1532	11	BC033727 Homo sapi
	10	735.2	26.7	788	9	AI951556 AI951556 wv36f04.x
c	11	722.8	26.3	843	13	BX348193 BX348193
	12	716.4	26.0	818	12	BI818609 603033362
	13	692	25.1	909	13	BX364574 BX364574
	14	678.2	24.6	2532	29	AY411748 Pan trogl
	15	672.6	24.4	934	10	BF311804 601897316
	16	666	24.2	939	13	BX345406 BX345406
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	22	610.2	22.2	2775	29	AY401471 Mus muscu
	23	607	22.1	889	13	BQ691915 AGENCOURT
	24	599	21.8	2775	29	AY401469 Homo sapi
	25	596.4	21.7	662	9	AL516580 AL516580
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## ALIGNMENTS

## RESULT 1

AY406491

LOCUS AY406491 2802 bp DNA linear GSS 15-DEC-2003

DEFINITION Homo sapiens UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY406491

VERSION AY406491.1 GI:39762465

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2802)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2802)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"

gene <1..>2802  
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## ORIGIN

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Best Local Similarity 61.3%; Pred. No. 1.2e-153;

Matches 1682; Conservative 0; Mismatches 995; Indels 69; Gaps 6;

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Qy      57  GCGGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGG 116
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Qy     117  TGCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCC 176
      || | | | | | | | | ||| || | || | || ||
Db     126  TGATGACTTTTTTCATGAACCTCCAGAACTTTTCCTTCTGATCCACCTGAGCCTCTGCC 185

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Qy 177 CCACTTCCTGGTGGAGCCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGT 236  
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 Qy 237 GTGCAAGGCCGTGCCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCA 296  
 Db 246 CTGTAAAGCAAGCCCTGCCACCCAGATCTATTTCAAGTGTAAATAGTGAATGGGTTTCATCA 305  
 Qy 297 GGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCACCATGGAGGT 356  
 Db 306 GAAGGACCACATAGTAGATGAAAGAGTAGATGAAACTTCCGGTCTCATTGTCCGGGAAGT 365  
 Qy 357 CCGCATTAAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCCGGGCTGGAGGAATACTGGTG 416  
 Db 366 GAGCATTGAGATTTTCGCGCCAGCAAGTGGAAGAACTCTTTGGACCTGAAGATTACTGGTG 425  
 Qy 417 CCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCAT 476  
 Db 426 CCAGTGTGTGGCCTGGAGCTCCGCGGGTACCACAAAGAGCCGGAAGGCGTATGTGCGCAT 485  
 Qy 477 AGC-----CAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCT 530  
 Db 486 TGCATNNNNNNNNNNNCGGAAGACATTTGAGCAGGAACCCCTAGGAAAGGAAGTGTCTTT 545  
 Qy 531 GGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGA 590  
 Db 546 GGAACAGGAAGTCTTACTCCAGTGTGACACCTGAAGGGATCCAGTGGCTGAGGTGGA 605  
 Qy 591 GTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCG 650  
 Db 606 ATGGTTGAAAAATGAAGACATAATTGATCCCGTTGAAGATCGGAATTTTATATTACTAT 665  
 Qy 651 GGAGCACAGCCTGGTGGTGGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGT 710  
 Db 666 TGATCACAACTCATCATAAAGCAGGCCGACTCTCTGATACTGCAAATTACACCTGTGT 725  
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 Db 786 CGGTGGCTGGTCCACCTGGACGGAGTGGTCTGTGTGTAAACAGCCGCTGTGGACGAGGGTA 845  
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 Db 846 TCAGAAACGTACAAGGACTTGTACCAACCCGGCACCCTCAATGGGGGTGCCTTCTGTGA 905  
 Qy 891 GGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCAGTAGACGGCAGCTGGAG 950  
 Db 906 AGGGCAGAGTGTGCAGAAAATAGCCTGTACTACGTTATGCCAGTGGATGGCAGGTGGAC 965  
 Qy 951 CCCGTGGAGCAAGTGGTTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTG 1010  
 Db 966 GCCATGGAGCAAGTGGTCTACTTGTGGAACAGTGTGCACCCACTGGCGCAGGAGGGAGTG 1025



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Db	1026	CACGGCGCCAGCCCCCAAGAATGGAGGCAAGGACTGCGACGGCCTCGTCTTGCAATCCAA	1085
Qy	1071	CAACTGTACCACTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTA	1130
Db	1086	GAAGTGCAGTGTATGGGCTTTGCATGCAGACTGCTCCTGATTCAGATGATGTTGCTCTCTA	1145
Qy	1131	TGTGGG---CCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCTCATCT	1187
Db	1146	TGTTGGGATTGTGATAGCAGTGATCGTTTGCCTGGCGATCTCTGTAGTTGTGGCCTTGTT	1205
Qy	1188	CGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCAC	1247
Db	1206	TGTGTATCGGAAGAATCATCGTGACTTTGAGTCAGATATTATTGACTCTTCGGCACTCAA	1265
Qy	1248	CTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCAC	1307
Db	1266	TGGGGGCTTTTTCAGCCTGTGAACATCAAG-----GCAGCAAGACAAGATCTGCTGGC	1316
Qy	1308	CATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCA	1367
Db	1317	TGTACCCCCAGACCTCACGTCAGCTGCAGCCATGTACAGAGGACCTGTCTATGCCCTGCA	1376
Qy	1368	GGATG-----GGCCCAGCCCCAAGTTCAGCTCACCAAT----GGGCACCTGCTCAGCCC	1418
Db	1377	TGACGTCTCAGACAAAATCCCAATGACCAACTCTCCAATTCTGGATCCACTGCCAACCT	1436
Qy	1419	CCTGGGTGGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTT	1478
Db	1437	GAAAATCAAAGTGTACAACACCTCAGGTGCTGTCAACCCCCAAGATGACCTCTCTGAGTT	1496
Qy	1479	CGTCTCCCGCCTCTCCACCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACAT	1538
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Qy	1539	GA-----CCTATGGGACCTTCAA	1556
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Qy	1617	TGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGT	1676
Db	1677	GGCCATTCCCCAAGGGAGAGTCTACGAAATGTATGTGACTGTACACAGGAAAGAACTAT	1736
Qy	1677	GAGGTTGCCCCCTAGCTGGCTGTGAGACCTGCTGAGTCCCATCGTTAGCTGTGGACCCCC	1736
Db	1737	GAGGCCACCCATGGATGACTCTCAGACACTTTTGACCCCTGTGGTGAGCTGTGGGCCCC	1796
Qy	1737	TGGCGTCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCC	1796
Db	1797	AGGAGCTCTGCTCACCCGCCAGTCGTCTCTCACTATGCATCACTGCGCAGACCCCAATAC	1856
Qy	1797	TGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCT	1856

Db	1857	CGAGGACTGGAAAATACTGCTCAAGAACCAGGCAGCACAGGGACAGTGGGAGGATGTGGT	1916
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Db	1917	GGTGGTCGGGGAGGAAAACCTCACCACCCCTGCTACATTCAGCTGGATGCAGAGGCCCTG	1976
Qy	1917	CTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGC	1976
Db	1977	CCACATCCTCACAGAGAACCTCAGCACCTACGCCCTGGTAGGACATTCCACCACCAAAGC	2036
Qy	1977	TGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGGCGCCGGTGGCCTGCACCTCCCTCGAGTA	2036
Db	2037	GGCTGCGAAGCGCCTCAAGCTGGCCATCTTTGGGCCCTGTGCTGCTCCTCGCTGGAGTA	2096
Qy	2037	CAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCT	2096
Db	2097	CAGCATCCGAGTCTACTGTCTGGATGACACCCAGGATGCCCTGAAGGAAATTTTACATCT	2156
Qy	2097	GGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTCAAGGACAG	2156
Db	2157	TGAGAGACAGATGGGAGGACAGCTCCTAGAAGAACCTAAGGCTCTTCATTTTAAAGGCAG	2216
Qy	2157	TTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCT	2216
Db	2217	CACCCACAACCTGCGCCTGTCAATTACGATATCGCCCATTCCCTCTGGAAGAGCAAATT	2276
Qy	2217	CCTTGTGCTAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCAGCGCGGTACTT	2276
Db	2277	GCTGGCTAAATATCAGGAAATTCCATTTTACCATGTTTGGAGTGGATCTCAAAGAAACCT	2336
Qy	2277	GCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCT	2336
Db	2337	GCACTGCACCTTCACTCTGGAAAGATTTAGCCTGAACACAGTGGAGCTGGTTTGCAAACCT	2396
Qy	2337	GTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAA	2396
Db	2397	CTGTGTGCGGCAGGTGGAAGGAGAAGGGCAGATCTTCCAGCTCAACTGCACCGTGTGAGA	2456
Qy	2397	GGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGT	2456
Db	2457	GGAACCTACTGGCATCGATTTGCCGCTGCTGGATCCTGCGAACACCATCACCACGGTCAC	2516
Qy	2457	GGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGA	2516
Db	2517	GGGGCCCAGTGCTTTCAGCATCCCTCTCCCTATCCGGCAGAAGCTCTGTAGCAGCCTGGA	2576
Qy	2517	CCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAG	2576
Db	2577	TGCCCCCAGACGAGAGGCCATGACTGGAGGATGCTGGCCATAAGCTGAACCTGGACAG	2636
Qy	2577	CCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGA	2636
Db	2637	GTACTTGAATTACTTTGCCACCAAATCCAGCCCAACTGGCGTAATCCTGGATCTTTGGGA	2696
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Db      2697 AGCACAGAACTTCCCAGATGGAAACCTGAGCATGCTGGCAGCTGTCTTGGAAGAAATGGG 2756
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# RESULT 2

AY406493

LOCUS AY406493 2791 bp DNA linear GSS 15-DEC-2003

DEFINITION Mus musculus UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY406493

VERSION AY406493.1 GI:39762467

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 2791)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2791)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

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gene        <1..>2791
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              /locus_tag="HCM2575"

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## ORIGIN

Query Match 34.5%; Score 950.4; DB 29; Length 2791;  
 Best Local Similarity 62.3%; Pred. No. 5.6e-152;  
 Matches 1653; Conservative 0; Mismatches 921; Indels 80; Gaps 7;

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 Db 398 AACTGTTTGGGCCTGAAGATTACTGGTGCCAGTGTGTGGCCTGGAGCTCAGCAGGCACTA 457  
 Qy 449 CCAAGAGTCAAGAAGGCCTACATCCGCATAGCCAG-----ATTGCGCAAGAACTTCGAGC 502  
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 Db 807 TGTGTAACAGCCGCTGTGGGCGAGGATATCAGAAACGCACAAGAACCTGCACCAACCCAG 866  
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Qy	1103	CTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGG---CCTCATCGCCGTGGCCGTCTGCC	1159
Db	1107	CTCCTGACTCAGATGATGTGGCTCTCTACGTGGGGATTGTGATCGCTGTAACAGTCTGTC	1166
Qy	1160	TGGTCCTGCTGCTGCTTGTCTCATCCTCGTTTATTGCCGAAGAAGGAGGGGCTGGACT	1219
Db	1167	TGGCGATCACTGTTGTGGTGGCCCTGTTTGTGTATCGGAAGAACCACCGTGACTTTGAGT	1226
Qy	1220	CAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCA	1279
Db	1227	CTGACATCATTGACTCCTCAGCACTCAATGGCGGCTTTCAGCCTGTGAACATCAAG----	1282
Qy	1280	GCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCGGACCTCAGCACCACCACCACCA	1339
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Qy	1340	CCTACCAGGGCAGTCTCTGTCCCCGGCAGGATG-----GGCCCAGCCCCAAGTTCCAGCT	1394
Db	1338	TGTACAGGGGACCTGTCTATGCTCTGCATGATGTCTCAGACAAAATCCCAATGACCAACT	1397
Qy	1395	CACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACACACTGCACCACAGCTC	1454
Db	1398	CTCCAATTCTGGACCCACTACCCAACCTTGAAAAATCAAAGTGTAACAGCTCAGGTGCTG	1457
Qy	1455	TCCCACCTC---TGAGGCCGAGGAGTTTCGTCTCCCGCCTCTCCACCC-----	1498
Db	1458	TCACTCCTCAGGATGACCTTGCCGAGTTCTCATCCAACTGTCACCCAGATGACCCAGT	1517
Qy	1499	-----AGAACTACTTCCGCTCCCTGCCCCGAGGCA	1528
Db	1518	CCTTGCTAGAGAATGAGGCCCTTAACCTGAAGAACCAGAGCCTCGCAAGACAGACTGACC	1577
Qy	1529	CCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATA	1588
Db	1578	CATCCTGCACAGCATTTGGTACCTTCAACTCTCTTGGGGGTACCTCATCATTCCTAATT	1637
Qy	1589	CAGGTATCAGCCTCCTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCT	1648
Db	1638	CAGGAGTAAGCTTGCTGATTCCCGCTGGGGCCATTCTCAGGGGAGAGTCTATGAAATGT	1697
Qy	1649	ACCTCACGCTGCACAAGCCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGC	1708
Db	1698	ATGTGACTGTACACAGGAAAGAAAATATGAGGCCCCCATGGAAGACTCTCAGACCCTAC	1757
Qy	1709	TGAGTCCCATCGTTAGCTGTGGACCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGG	1768
Db	1758	TTACCCCTGTGGTGAAGCTGTGGGCCCTCTGGAGCTCTGCTGACCCGCCCTGTATCCTCA	1817
Qy	1769	CTATGGACCACTGTGGGGAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGT	1828
Db	1818	CTCTGCATCACTGTGCAGACCCAGACCCGAGGACTGGAAGATCCAGCTCAAAAACCAGG	1877
Qy	1829	CGTGCGAGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCT	1888
Db	1878	CAGTGCAGGGACAATGGGAGGATGTTGTGGTGGTTGGGGAGGAGAAGTTCAACCCCCCT	1937

Qy 1889 ACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTG 1948  
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 Db 1938 GTTACATTACAGCTGGATGCAGAGGCTTGCCATATCCTCACAGAGAACCTCAGTACCTATG 1997  
 Qy 1949 CCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTG 2008  
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 Qy 2009 CGCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCC 2068  
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 Qy 2069 ACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGACAGCTGATCCAGG 2128  
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 Db 2718 TGCTGGCAGCCGTCCTGGAAGAAATGGGAAGACATGAGACAGTGGTGTCTTGGCAGCAG 2777

Qy 2729 AGGCTGAGTGCTGA 2742  
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 Db 2778 AAGGACAGTATTGA 2791

# RESULT 3

AK031655

LOCUS AK031655 3790 bp mRNA linear HTC 18-SEP-2003

DEFINITION Mus musculus 13 days embryo male testis cDNA, RIKEN full-length enriched library, clone:6030473H24 product:unc5 homolog (C. elegans) 3, full insert sequence.

ACCESSION AK031655

VERSION AK031655.1 GI:26327502

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

## REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

## REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

## REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

## REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 3790)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source 1. .3790  
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/clone\_lib="RIKEN full-length enriched mouse cDNA library"  
/dev\_stage="13 days embryo"

CDS 118. .2970  
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/db\_xref="GI:26327503"  
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ORIGIN

Query Match 33.6%; Score 923.4; DB 11; Length 3790;  
 Best Local Similarity 61.3%; Pred. No. 2.7e-147;  
 Matches 1659; Conservative 0; Mismatches 926; Indels 120; Gaps 6;

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Qy	209	TCGTCAAGAACAAGCCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCT	268
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Qy	329	GGAGCAGTGGGCTGCCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTGAGAG	388
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Qy	449	CCAAGAGTCAGAAGGCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGC	508
Db	575	CGAAGAGTCGGAAGGCATACGTGCGCATTGCGTATCTGCGGAAGACATTCGAGCAGGAAC	634
Qy	509	CGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGG	568
Db	635	CCTTGGGAAAGGAAGTGTCTTGGAGCAGGAAGTCTTACTCCAGTGTCGGCCACCTGAAG	694
Qy	569	GCATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGG	628
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Qy	749	CTGCTGTTCATCGTCTACGTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCGTCTGCA	808
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Qy	809	GCGCCAGCTGTGGGCGCGGCTTGGCAGAAAACGGAGCCGGAGCTGCACCAACCCGCGCCTC	868
Db	935	ACAGCCGCTGTGGGCGAGGATATCAGAAACGCACAAGAACCTGCACCAACCCAGCCCCAC	994
Qy	869	TCAACGGGGGCGCTTTCTGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGT	928
Db	995	TCAATGGTGGGGCCTTCTGTGAGGGGCAGAGTGTGCAGAAAATAGCATGCACTACGTTAT	1054
Qy	929	GCCCAGTAGACGGCAGCTGGAGCCCGTGGAGCAAAGTGGTCGGCCTGTGGGCTGGACTGCA	988
Db	1055	GTCCAGTGGATGGTAGGTGGACTTCATGGAGCAAATGGTCAACCTGTGGGACTGAATGCA	1114
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Db	1175	ATGGCCTGGTCTCCAATCCAAGAACTGCACTGATGGGCTGTGCATGCAGGGATTTCATTT	1234
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Qy	1112	CTGAGGACGTGGCCCTCTATGTGGG---CCTCATCGCCGTGGCCGTCTGCCTGGTCTCTGC	1168
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Qy	1169	TGCTGCTTGTCTCATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGG	1228
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Qy	1229	CTGACTCGTCCATTCTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAG	1288
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Qy	1289	ACAACCCCCATCTGCTCACCATCCAGCCGGACCTCAGCACCACCACCACCCTACCAGG	1348
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Qy	1349	GCAGTCTCTGTCCCCGGCAGGATG-----GGCCAGCCCCAAGTTCAGCTCACCAATGG	1403
Db	1526	GACCTGTCTATGCTCTGCATGATGTCTCAGACAAAATCCCAATGACCAACTCTCCAATTC	1585
Qy	1404	GCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACACACTGCACCACAGCTCTCCCACCTC	1463
Db	1586	TGGACCCACTACCCAACCTTGAAAATCAAAGTGTAACAGCTCAGGTGCTGTCACTCCTC	1645
Qy	1464	----TGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCC-----	1498
Db	1646	AGGATGACCTTGCCGAGTTCTCATCAAACCTGTCACCCAGATGACCCAGTCCTTGCTAG	1705
Qy	1499	-----AGAACTACTTCCGCTCCCTGCCCGAGGCACCAGCAACA	1537
Db	1706	AGAATGAGGCCCTTAACCTGAAGAACCAGAGCCTCGCAAGACAGACTGACCCATCCTGCA	1765

Qy 1538 TGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCA 1597  
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 Db 1766 CAGCATTTGGTACCTTCAACTCTCTTGGGGGTACCTCATCATTCCTAATTCAGGAGTAA 1825

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 Db 1826 GCTTGCTGATTCCCGCTGGGGCCATTCTCAGGGGAGAGTCTATGAAATGTATGTGACTG 1885

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 Db 1886 TACACAGGAAAGAAAATATGAGGCCCCCATGGAAGACTCTCAGACCCCTACTTACCCCTG 1945

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 Db 1946 TGGTGAGCTGTGGGCCTCTGGAGCTCTGCTGACCCGCCCTGTCATCTCACTCTGCATC 2005

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 Db 2006 ACTGTGCAGACCCAGCACCGAGGACTGGAAGATCCAGCTCAAAAACCAGGCAGTGCAGG 2065

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Qy 1898 AGCTGGAGGCCAGTGCCTGCTACGTCTTACCGAGCAGCTGGGCCGCTTTGCCCTGGTGG 1957  
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Qy 1958 GAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGG 2017  
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Qy 2078 TCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGACAGCTGATCCAGGAGCCACGGG 2137  
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Qy 2138 TCCTGCACTTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCT 2197  
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 Db 2366 CTCTTCGTTTTAAAGGCAGCATCCACAACCTGCGCCTGTCTATTCATGACATCGCCATT 2425

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Db      2606 TCAACTGTACTGTGTCTCAGAGGAACCTACTGGCATCGACTTACCTCTCCTGGACCCTGCTA 2665
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Qy      2558 AGAAACTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCA 2617
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Qy      2618 TGATCCTCAACCTGTGGGAGGCGCGGCACCTCCCCAACGGCAACCTCAGCCAGCTGGCTG 2677
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Db      2906 CCGTCCTGGAAGAAATGGGAAGACATGAGACAGTGGTGTACTTGGCAGCAGAAGGACAGT 2965
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Db      2966 ATTGA 2970

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#### RESULT 4

AK018177

LOCUS AK018177 3866 bp mRNA linear HTC 20-SEP-2003

DEFINITION Mus musculus adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330415E02 product:TRANSMEMBRANE RECEPTOR UNC5H2 homolog [Rattus norvegicus], full insert sequence.

ACCESSION AK018177

VERSION AK018177.1 GI:12857775

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

#### REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

#### REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

#### REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,

Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 3866)

AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCC 3']. cDNA was cleaved

with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.

FEATURES  
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ORIGIN

Query Match                      31.7%;    Score 872.4;    DB 11;    Length 3866;  
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Qy            157    GCCAACCCGGACCTGCTTCCCCACTTCTGGTGGAGCCCGAGGATGTGTACATCGTCAAG    216  
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Qy            217    AACAAAGCCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGC    276  
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Db            600    AACAAAGCCAGTGGAAGTGCAGTGCAGAGCCTTCCCTGCCACGCAGATCTACTTCAAGTGT    659  
  
Qy            277    AACGGGGAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGT    336  
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Qy	397	GGGCTGGAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGT	456
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Qy	997	CGGAGCCGTGAGTGTCTGACCCAGCACCCCCGCAACGGAGGGGAGGAGTGCCAGGGCACT	1056
Db	1380	CGCAGCCGCGAGTGCATGGCACCCGCCACCCCAGAACGGAGGCCGTGACTGCAGCGGGACG	1439
Qy	1057	GACCTGGACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCC-----	1111
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RESULT 5

AY406492

LOCUS AY406492 2802 bp DNA linear GSS 15-DEC-2003

DEFINITION Pan troglodytes UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY406492

VERSION AY406492.1 GI:39762466

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 2802)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2802)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

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ORIGIN

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Qy     117  TGCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCC 176
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Db	306	NN	365
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Db	426	NN	485
Qy	471	CCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCT	530
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Qy	891	GGGGCAGAAATGTCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGCTGGAG	950
Db	906	AGGGCAGAGTGTGCAGAAAATAGCCTGTACTACGTTATGCCCAGTGGATGGCAGGTGGAC	965
Qy	951	CCCGTGGAGCAAGTGGTTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTG	1010
Db	966	GCCATGGAGCAAGTGGTCTACTTGTGGAACAGTGTGCACCCACTGGCGCAGGAGGGAGTG	1025
Qy	1011	CTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCG	1070

Db	1026	CACGGCGCCAGCCCCCAAGAATGGAGGCAAGGACTGCGATGGCCTCGTCTTGCAATCCAA	1085
Qy	1071	CAACTGTACCACTGACCTCTGTGTACACAGTGTCTTGGCCCTGAGGACGTGGCCCTCTA	1130
Db	1086	GAAGTGCAGTGTATGGGCTTTGCATGCAGACTGCTCCTGATTGATGATGTTGCTCTCTA	1145
Qy	1131	TGTGGG---CCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCATCCT	1187
Db	1146	TGTTGGGATTGTGATAGCAGTGATCGTTTGCCTGGCGATCTCTGTAGTTGTGGCCTTGTT	1205
Qy	1188	CGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCAC	1247
Db	1206	TGTGTATCGGAAGAATCATCGTGACTTTGAGTCAGATATTATTGACTCTTCGGCACTCAA	1265
Qy	1248	CTCAGGCTTCCAGCCCGTCAGCATCAAGCCAGCAAAGCAGACAACCCCCATCTGCTCAC	1307
Db	1266	TGGGGGCTTTTCAGCCTGTGAACATCAAG-----GCAGCAAGACAAGATCTGCTGGC	1316
Qy	1308	CATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCA	1367
Db	1317	TGTACCCCCAGACCTCACGTCAGCTGCAGCCATGTACAGAGGACCTGTCTATGCCCTGCA	1376
Qy	1368	GGATG-----GGCCCAGCCCCAAGTTCAGCTCACCAAT----GGGCACCTGCTCAGCCC	1418
Db	1377	TGACGTCTCAGACAAAATCCCAATGACCAACTCTCCAATTCTGGATCCACTGCCAACCT	1436
Qy	1419	CCTGGGTGGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTT	1478
Db	1437	GAAAATCAAAGTGTACAACACCTCAGGTGCTGTCAACCCCCAAGATGACCTCTCTGAGTT	1496
Qy	1479	CGTCTCCCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACAT	1538
Db	1497	TACGTCCAAGCTGTCCCTCAGATGACCCAGTCATTGTTGGAGAATGAAGCCCTCAGCCT	1556
Qy	1539	GA-----CCTATGGGACCTTCAA	1556
Db	1557	GAAGAACCAGAGTCTAGCAAGGCAGACTGATCCATCCTGTACCGCATTGGCAGCTTCNN	1616
Qy	1557	CTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGA	1616
Db	1617	NTNGCTGGGNNNNCACCTTATTGTTCCCAATTCAGGAGTCAGCTTGCTGATTCCCCTGG	1676
Qy	1617	TGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCAGCTGCACAAGCCGGAAGACGT	1676
Db	1677	GGCCATTCCCCAAGGGAGAGTCTACGAAATGTATGTGACTGTACACAGGAAAGAACTAT	1736
Qy	1677	GAGGTTGCCCCTAGCTGGCTGTCAGACCTGCTGAGTCCCATCGTTAGCTGTGGACCCCC	1736
Db	1737	GAGGCCACCCATGGATGACTCTCAGACACTTTTGACCCCTGTGGTGAGCTGTGGGCCCC	1796
Qy	1737	TGGCGTCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCC	1796
Db	1797	AGGAGCTCTGCTCACCCGCCCGTCGTCTTACTATGCATCACTGCGCAGACCCCAATAC	1856
Qy	1797	TGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCT	1856

Db 1857 CGAGGACTGGAAAATACTGCTCAAGAACCAGGCAGCACAGGGACAGTGGGAGGATGTGGT 1916

Qy 1857 GCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTG 1916  
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Db 1917 GGTGGTCGGGGAGGAAAACCTCACCACCCCTGCTACATTCAGCTGGATGCAGAGGCCTG 1976

Qy 1917 CTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGC 1976  
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Db 1977 CCACATCCTCACAGAGAACCTCAGCACCTACGCCCTGGTAGGACATTCCACCACCAAAGC 2036

Qy 1977 TGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTA 2036  
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Db 2037 GGCTGCGAAGCGCCTCAAGCTGGCCATCTTTGGGCCCTGTGCTGCTCCTCGCTGGAGTA 2096

Qy 2037 CAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCT 2096  
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Db 2097 CAGCATCCGAGTCTACTGTCTGGATGACACCAGGATGCCCTGAAGGAAATTTTACATCT 2156

Qy 2097 GGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTCAAGGACAG 2156  
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Db 2157 TGAGAGACAGATGGGAGGACAGCTCCTAGAAGAACCTAAGGCTCTTCATTTTAAAGGCAG 2216

Qy 2157 TTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCT 2216  
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Db 2217 CACCCACAACCTGCGCCTGTCAATTACGATATCGCCCATTCCTCTGGAAGAGCAAATT 2276

Qy 2217 CCTTGTCAGCTACCAGGAGATCCCCCTTTATCACATCTGGAATGGCAGCAGCGGTACTT 2276  
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Db 2277 GCTGGCTAAATATCAGNNNAACCT 2336

Qy 2277 GCACTGCACCTTCACCTGGAGCGTGTGAGCCCAGCACTAGTGACCTGGCCTGCAAGCT 2336  
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Db 2337 GCACTGCACCTTCACTCTGGAAGATTAGCCTGAACACAGTGGAGCTGGTTTGCAAAC 2396

Qy 2337 GTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAA 2396  
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Db 2397 CTGTGTGCGGCAGGTGGAAGGAGAAGGGCAGATCTTCAGCTCAACTGCACCGTGTGAGA 2456

Qy 2397 GGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGT 2456  
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Db 2457 GGAACCTACTGGCATCGATTTGCCGCTGCTGGATCCTGCGAACACCATCACACGGTCAC 2516

Qy 2457 GGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGA 2516  
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Db 2517 GGGGCCAGTGCTTTCAGCATCCCTCTCCCTATCCGGCAGAAGCTCTGTAGCAGCCTGGA 2576

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Db 2577 TGCCCCCAGACGAGAGGCCATGACTGGAGGATGCTGGCCCATAAGCNNNNNNNNNNNN 2636

Qy 2577 CCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGA 2636  
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Db 2637 GTACTTGAATTACTTTGCCACCAAATCCAGCCCAACTGGCGTAATCCTGGATCTTTGGGA 2696

Qy 2637 GGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGG 2696  
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Db 2697 AGCACAGAACTTCCCAGATGGAAACCTGAGCATGCTGGCAGCTGTCTTGGAAGAAATGGG 2756

Qy 2697 CCAGCCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGA 2742  
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 Db 2757 AAGACATGAAACGGTGGTGTCTTAGCAGCAGAAGGGCAGTATTAA 2802

## RESULT 6

AY411747

LOCUS AY411747 2532 bp DNA linear GSS 12-DEC-2003

DEFINITION Homo sapiens HCM4327 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY411747

VERSION AY411747.1 GI:39767715

**KEYWORDS** GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2532)

AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

TITLE      Inferring nonneutral evolution from human-chimp-mouse orthologous  
             gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2532)

AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES	Location/Qualifiers
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            /organism="Homo sapiens"  
            /mol_type="genomic DNA"  
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gene        <1..>2532  
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## ORIGIN

Query Match 29.4%; Score 810.4; DB 29; Length 2532;

Best Local Similarity 61.1%; Pred. No. 4.6e-128;

Matches 1540; Conservative 0; Mismatches 851; Indels 129; Gaps 9;

QY 352 GAGGTCCGCATTAATGTCTCAAGGCAGCAGGTTCGAGAAGGTGTTCTGGGCTGGAGGAATAC 411  
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Db 13 GAGGTGCAGATCGAGGTGTCGCGGCAGCAGGTGGAGGAGCTCTTTGGGCTGGAGGATTAC 72

QY            412 TGGTGCCAGTGCCTGGCATGGAGCTCCTCGGGCACCAAGAGTCAGAAGGCCCTACATC     471  
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Db 73 TGGTGCCAGTGCGTGGCCTGGAGCTCCGCGGGCACCACCAAGAGTCGCCGAGCCTACGTC 132

Qy 472 CGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTG 531  
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 Db 133 CGCATCGCCTACCTGCGCAAGAACTTCGATCAGGAGCCTCTGGGCAAGGAGGTGCCCTG 192

Qy 532 GAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAG 591  
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 Db 193 GACCATGAGGTTCCTGCACTGCCGCCCGCCGGAGGGGTGCCTGTGGCCGAGGTGGAA 252

Qy 592 TGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGG 651  
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 Db 253 TGGCTCAAGAATGAGGATGTCATCGACCCACCCAGGACACCAACTTCCTGCTCACCATC 312

Qy 652 GAGCACAGCCTGGTGGTGCACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGTG 711  
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 Db 313 GACCACAACCTCATCATCCGCCAGGCCCGCCTGTGCGACACTGCCAACTATACCTGCGTG 372

Qy 712 GCCAAGAACATCGTGGCACGTGCGCGCAGCGCCTCCGCTGCTGTCATCGTCTACGTGAAC 771  
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 Db 373 GCCAAGAACATCGTGGCCAAACGCCGGAGCACCCTGCCACCGTCATCGTCTACGTGAAT 432

Qy 772 GGTGGGTGGTGCACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGG 831  
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 Db 433 GGCGGCTGGTCCAGCTGGGCAGAGTGGTCACCCTGCTCCAACCGCTGTGGCCGAGGCTGG 492

Qy 832 CAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTCTGTGAG 891  
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 Db 493 CAGAAGCGCACCCGGACCTGCACCAACCCCGCTCCACTCAACGGAGGGGCGCTTCTGCGAG 552

Qy 892 GGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGCTGGAGC 951  
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 Db 553 GGCCAGGCATTCAGAAAGACCGCTGCACCACCATCTGCCCAGTCGATGGGGCGTGGACG 612

Qy 952 CCGTGGAGCAAGTGGTTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGC 1011  
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 Db 613 GAGTGGAGCAAGTGGTTCAGCCTGCAGCACTGAGTGTGCCCACTGGCGTAGCCGCGAGTGC 672

Qy 1012 TCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGC 1071  
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 Db 673 ATGGCGCCCCCACCACAGAACGGAGGCCGTGACTGCAGCGGGACGCTGCTCGACTCTAAG 732

Qy 1072 AACTGTACCAGTGACCTCTGTGTACACAGTGCTTCT----- 1107  
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 Db 733 AACTGCACAGATGGGCTGTGCATGCAAAATAAGAAAACCTCTAAGCGACCCCAACAGCCAC 792

Qy 1108 -----GGCCCTGAGGACGTGGCCCTCTATGTGGGCCTC---ATCGCCGTGGCCGTC 1155  
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 Db 793 CTGCTGGAGGCCTCAGGGGATGCGGCGCTGTATGCGGGGCTCGTGGTGGCCATCTTCGTG 852

Qy 1156 TGCCTGGTCCTGCTGCTGTCTCCTCATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTG 1215  
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 Db 853 GTCGTGGCAATCCTCATGGCGGTGGGGGTGGTGGTGTACCGCCGCAACTGCCGTGACTTC 912

Qy 1216 GACTCAGATGTGGCTGACTCGTCCATT---CTCACCTCAGGCTTCCAGCCCGTCAGCATC 1272  
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 Db 913 GACACAGACATCACTGACTCATCTGCTGCCCTGACTGGTGGTTTCCACCCCGTCAACTTT 972

Qy 1273 AAGCCCAGCAAAGCAGACAACCCCCATCTGCT-----CACCATCCAGCCGGACCTCAGC 1326  
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 Db 973 AAGACGGCAAGGCCAGCAACCCGCAGCTCCTACACCCCTCTGTGCCTCCTGACCTGACA 1032

Qy 1327 ACCACCACCACCACCTACCAGGCGAGTCTCTGTCCCCGGCAGGATGGG----- 1374  
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 Db 1033 GCCAGCGCCGGCATCTACCGCGGACCCGTGTATGCCCTGCAGGACTCCACCGACAAAATC 1092

Qy 1375 -----CCCAGCCCCAAGTTCCAGCTCACCA-- 1399  
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 Db 1093 CCCATGACCAACTCTCCTCTGCTGGACCCCTTACCCAGCCTTAAGGTCAAGGTCTACAGC 1152

Qy 1400 -----ATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCC-----ACACA 1440  
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Qy 1441 CTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAG 1500  
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Qy 1501 AACTACTTCCGCTC-----CCTGCCCCGAGGCACCAGCAACATGACCTAT 1545  
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 Db 1273 GCCAGCCTCGGTTCCCAGCAGCTCTTGGGCCTGCCCCGAGACCCAGGGAGCAGCGTCAGC 1332

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 Db 1333 GGCACCTTTGGCTGCCTGGGTGGGAGGCTCAGCATCCCCGGCACAGGGGTGAGCTTGCTG 1392

Qy 1606 ATCCCCCAGATGCCATACCCCCGAGGGAAGATCTATGAGATCTACCTCAGCTGCACAAG 1665  
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Qy 1666 CCGGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGC 1725  
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Qy 1726 TGTGGACCCCCTGGCGTCTGCTCACC CGCCAGTCATCCTGGCTATGGACCACTGTGGG 1785  
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 Db 1513 TGTGGACCCACAGGCCTCCTGCTGTGCCGCCCCGTATCCTCACCATGCCCCACTGTGCC 1572

Qy 1786 GAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG 1845  
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 Db 1573 GAAGTCAGTGCCCGTGACTGGATCTTTCAGCTCAAGACCCAGGCCACCAGGGCCACTGG 1632

Qy 1846 GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAG 1905  
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 Db 1633 GAGGAGGTGGTGACCCTGGATGAGGAGACCCTGAACACACCCTGCTACTGCCAGCTGGAG 1692

Qy 1906 GCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCC 1965  
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 Db 1693 CCCAGGGCCTGTCACATCCTGCTGGACCAGCTGGGCACCTACGTGTTACGGGCGAGTCC 1752

Qy 1966 CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC 2025  
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Qy 2026 TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG 2085



Db	1813	TCCCTGGAGTACAGCCTCCGGGTCTACTGCCTGGAGGACACGCCTGTAGCACTGAAGGAG	1872
Qy	2086	GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTTGCAC	2145
Db	1873	GTGCTGGAGCTGGAGCGGACTCTGGGCGGATACTTGGTGGAGGAGCCGAAACCGCTAATG	1932
Qy	2146	TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGG	2205
Db	1933	TTCAAGGACAGTTACCACAACCTGCGCCTCTCCCTCCATGACCTCCCCCATGCCCATTTGG	1992
Qy	2206	AAGAGTAAGCTCCTTGTACAGTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCAGC	2265
Db	1993	AGGAGCAAGCTGCTGGCCAAATACCAGGAGATCCCCTTCTATCACATTTGGAGTGGCAGC	2052
Qy	2266	CAGCGGTACTTGCAGTGCACCTTCACCCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTG	2325
Db	2053	CAGAAGGCCCTCCACTGCACCTTTCACCCCTGGAGAGGCACAGCTTGGCCTCCACAGAGCTC	2112
Qy	2326	GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTC	2385
Db	2113	ACCTGCAAGATCTGCGTGCGGCAAGTGAAGGGGAGGGCCAGATATTCCAGCTGCATACC	2172
Qy	2386	AACATCACCAAG---GACACAAGGTTTGTCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGG	2442
Db	2173	ACTCTGGCAGAGACACCTGCTGGCTCCCTGGACACTCTCTGCTCTGCCCCTGGCAGCACT	2232
Qy	2443	GTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATA	2502
Db	2233	GTCACCACCCAGCTGGGACCTTATGCCTTCAAGATCCCACTGTCCATCGGCCAGAAGATA	2292
Qy	2503	ATTTCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAA	2562
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Qy	2563	CTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATC	2622
Db	2353	CTCTCTATGGACCGGTACCTGAATTACTTTGCCACCAAGCGAGCCCCACGGGTGTGATC	2412
Qy	2623	CTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCA	2682
Db	2413	CTGGACCTCTGGGAAGCTCTGCAGCAGGACGATGGGGACCTCAACAGCCTGGCGAGTGCC	2472
Qy	2683	GTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTGCGGAGGCTGAGTGCTGA	2742
Db	2473	TTGGAGGAGATGGGCAAGAGTGAGATGCTGGTGGCTGTGGCCACCGACGGGGACTGCTGA	2532

# RESULT 7

AY411749

LOCUS	AY411749	2532 bp	DNA	linear	GSS 12-DEC-2003
DEFINITION	Mus musculus HCM4327 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.				
ACCESSION	AY411749				
VERSION	AY411749.1 GI:39767717				
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 2532)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302

REFERENCE 2 (bases 1 to 2532)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.

TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.

FEATURES Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
gene <1..>2532  
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ORIGIN

Query Match 28.4%; Score 780.4; DB 29; Length 2532;  
Best Local Similarity 60.1%; Pred. No. 6.3e-123;  
Matches 1515; Conservative 0; Mismatches 876; Indels 129; Gaps 8;

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Db      13  GAGGTGCAGATCGAGGTGTCACGGCAGCAAGTGGAGGAACCTCTTCGGGCTCGAGGACTAC 72

Qy      412 TGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATC 471
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Qy      472 CGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTG 531
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Qy      532 GAGCAGGGCATCGTGCTGCCCTGCCGTCCACGGAGGGCATCCCTCCAGCCGAGGTGGAG 591
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Qy      592 TGGCTCCGGAACGAGGACCTGGTGGACCCGTCCTGGACCCCAATGTATACATCACGCGG 651
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Db      253 TGGCTCAAGAATGAAGATGTCATTGACCCCGCTCAGGACACTAACTTCCTGCTCACCATT 312

Qy      652 GAGCACAGCCTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGTG 711
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```

Db 313 GACCACAACCTCATCATCCGCCAGGCGCGCCTCTCAGACACGGCCAACTACACCTGTGTG 372

Qy 712 GCCAAGAACATCGTGGCACGTCGCCGAGCGCCTCCGCTGCTGTTCATCGTCTACGTGAAC 771  
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Db 373 GCCAAGAATATCGTGGCCAAGCGCCGAGCACCACGGCCACAGTCATCGTCTATGTGAAT 432

Qy 772 GGTGGGTGGTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGG 831  
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Db 433 GGAGGCTGGTCCAGCTGGGCAGAGTGGTCACCTGTTCCAATCGCTGTGGCCGAGGCTGG 492

Qy 832 CAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGCGCTTTCTGTGAG 891  
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Db 493 CAGAAGCGTACTCGGACCTGCACCAATCCAGCCCCACTCAATGGAGGCGCCTTCTGTGAG 552

Qy 892 GGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGCTGGAGC 951  
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Db 553 GGACAGGCCTTCCAGAAGACAGCTTGCACCACCGTGTGCCCAGTGGATGGAGCGTGGACC 612

Qy 952 CCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGC 1011  
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Db 613 GAGTGGAGCAAGTGGTCTGCCTGCAGCACAGAGTGTGCGCACTGGCGCAGCCGCGAGTGC 672

Qy 1012 TCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGC 1071  
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Db 673 ATGGCACC GCCACCCAGAACGGAGGCCGTGACTGCAGCGGGACGCTACTTGACTCCAAG 732

Qy 1072 AACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGAC----- 1119  
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Db 733 AACTGCACTGATGGGCTGTGCGTGTGAATCAGAGAACTCTAAACGACCCTAAAAGCCAC 792

Qy 1120 -----GTGGCCCTCTATGTGGGCCCTCATCGCCGTGGCCGTCTGC 1158  
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Db 793 CCCCTGGAGACATCGGGAGATGTGGCACTGTACGCAGGCCTTGTGGTGGCCGTCTTTGTG 852

Qy 1159 CTGGTCTCTGCTGCTTGTCTCT---CATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTG 1215  
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Db 853 GTGGTAGCGGTTCTCATGGCCGTGGGAGTGATCGTATACCGGAGAACTGCCGGGACTTC 912

Qy 1216 GACTCAGATGTGGCTGACTCGT---CCATTCTCACCTCAGGCTTCCAGCCCGTCAGCATC 1272  
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Db 913 GACACGGACATCACCGACTCCTCTGCGGCCCTCACTGGTGGCTTCCACCCTGTCAACTTC 972

Qy 1273 AAGCCCAGCAAAGCAGACAACCCCCATCTGCT-----CACCATCCAGCCGGACCTCAGC 1326  
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Db 973 AAGACTGCAAGGCCCAACAACCCGCAGCTCCTGCACCCGTCCGCCCCCTCCAGACCTAACG 1032

Qy 1327 ACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGG----- 1373  
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Db 1033 GCCAGTGCTGGCATCTACCGCGGGCCTGTGTATGCCCTGCAGGACTCCGCCGACAAGATC 1092

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Db 1093 CCCATGACTAATTGCCCCCTGCTGGATCCCCTGCCAGCCTCAAGATCAAGGTCTATAAC 1152

Qy 1402 GGGCACCTGCTCAG-----CCCCCTGGGTGGCGGC 1431  
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Qy	1546	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTC	1605
Db	1333	GGCACCTTTGGTTGCCTGGGAGGAAGGCTGAGCCTCCCCGGCACAGGGGTGAGCCTGTTG	1392
Qy	1606	ATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG	1665
Db	1393	GTACCAAATGGAGCCATTCCCCAGGGCAAGTTCTATGACCTGTATCTACATATCAACAAG	1452
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Db	1513	TGTGGGCCACAGGCCTACTCCTGTGCCGCCCTGTCGTCTCACCGTGCCCACTGTGCT	1572
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Db	1633	GAGGAGGTGGTGACCTTGGATGAGGAGACCCTCAACACACCCTGCTACTGCCAGCTGGAG	1692
Qy	1906	GCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCGCTTTGCCCTGGTGGGAGAGGCC	1965
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Qy	1966	CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC	2025
Db	1753	TACTCTCGCTCTGCAGTCAAGCGGCTCCAGCTGGCCATCTTCGCCCCAGCCCTCTGCACC	1812
Qy	2026	TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG	2085
Db	1813	TCCCTGGAGTATAGCCTCAGGGTCTACTGTCTGGAGGACACACCTGTAGCACTGAAGGAG	1872
Qy	2086	GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCAC	2145
Db	1873	GTCTTGGAGCTGGAGAGGACTCTGGGTGGCTACTTGGTGGAGGAGCCCAAGCCTTTGCTC	1932
Qy	2146	TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGG	2205
Db	1933	TTTAAGGACAGTTACCACAACCTACGCCTCTCCCTCCATGACATCCCCATGCCCACTGG	1992
Qy	2206	AAGAGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCCTTTTATCACATCTGGAATGGCAG	2265
Db	1993	AGGAGCAAACCTACTGGCCAAGTACCAGGAGATTCCCTTCTACCACGTCTGGAATGGCAGC	2052

Qy 2266 CAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTG 2325  
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Qy 2386 AACATCACC---AAGGACACAAGTTTGTCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGG 2442  
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 Db 2173 ACGTTGGCCGAGACGCCTGCTGGCTCCCTGGATGCTCTCTGCTCTGCCCCGGGCAATGCC 2232

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Qy 2503 ATTTCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAA 2562  
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Qy 2563 CTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATC 2622  
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Qy 2623 CTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCA 2682  
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Qy 2683 GTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTGCGAGGCTGAGTGCTGA 2742  
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# RESULT 8

BI758231

LOCUS BI758231 1034 bp mRNA linear EST 25-SEP-2001

DEFINITION 603029876F1 NIH\_MGC\_114 Homo sapiens cDNA clone IMAGE:5200171 5', mRNA sequence.

ACCESSION BI758231

VERSION BI758231.1 GI:15749809

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1034)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov  
Plate: LLAM11501 row: g column: 20  
High quality sequence stop: 793.

FEATURES  
source Location/Qualifiers  
1. .1034  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:5200171"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_114"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: EcoRV (destroyed); RNA source anonymous pool of 6  
male brains, age range 23-27 yo. Library is oligo-dT  
primed and directionally cloned (EcoRV site is destroyed  
upon cloning). Average insert size 1.5 kb, insert size  
range 1-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 019. Note:  
this is a NIH\_MGC Library."

ORIGIN

Query Match 27.9%; Score 768.6; DB 12; Length 1034;  
Best Local Similarity 91.2%; Pred. No. 4.3e-121;  
Matches 918; Conservative 0; Mismatches 74; Indels 15; Gaps 9;

Qy	150	GCCTGGTGCCAACCCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACAT	209
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Qy	210	CGTCAAGAACAAGCCAGTGCTGCTTGTGTGCAAGGCCGTGCCCCGCCACGCAGATCTTCTT	269
Db	61	CGTCAAGAACAAGCCAGTGCTGCTTGTGTGCAAGGCCGTGCCCCGCCACGCAGATCTTCTT	120
Qy	270	CAAGTGCAACGGGGAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGG	329
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Qy	330	GAGCAGTGGGCTGCCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAA	389
Db	181	GAGCAGTGGGCTGCCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAA	240
Qy	390	GGTGTTTCGGGCTGGAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCAC	449
Db	241	GGTGTTTCGGGCTGGAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCAC	300
Qy	450	CAAGAGTCAGAAGGCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCC	509
Db	301	CAAGAGTCAGAAGGCCTACATCCGCATAGCCTATTTGCGCAAGAACTTCGAGCAGGAGCC	360
Qy	510	GCTGGCCAAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGG	569
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Qy	570	CATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGA	629
Db	421	CATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGA	480

Qy 630 CCCCATGTATACATCACGCGGGAGCACAGCCTGGTGGTGCACAGGCCCGCCTTGCTGA 689  
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 Db 481 CCCCATGTATACATCACGCGGGAGCACAGCCTGGTGGTGCACAGGCCCGCCTTGCTGA 540  
 Qy 690 CACGGCCAACTACACCTGCGTGGCCAAGAACATCGTGGCACGTCGCCGACGCGCCTCCGC 749  
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 Db 601 TGCTGTCATCGTCTACGTGAACGGTGGGTGGTTCGACCGTGGACCGAGTGGTCCGTCTGC- 659  
 Qy 809 GCGCCAGCTGTGGGCGGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTC 868  
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 Db 660 GCGCCAGCTGTGGGCGGGCTGGCAGAAACGGAGCCGGAGCTGCACAACCCGGTGCCTC 719  
 Qy 869 TCAACGGGGGCGCTTTCTGTGA-GGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTG 927  
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 Db 720 TCAACGGGGGCGCTTTCTGTGAGGGGGCAGAATGTCCAGAAAGCAGC---TGCGCCACCT 776  
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 Db 837 GCACCCACTTGGGCGGAGCCGGAGTGCTCTGAACCCAGCACCCCGGCACGGCAGGGGGAG 896  
 Qy 1044 GTG---CCAGGGCACTGACCTGGACACCCGCAACTGTACCAGTGACCTCTGTGTACACAG 1100  
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 Db 955 GGGTTCTGGCCCTGAGGACTTGGCCCTCCTATGTGGGCCTCATCCCG 1001

# RESULT 9

BC033727

LOCUS BC033727 1532 bp mRNA linear HTC 19-NOV-2003

DEFINITION Homo sapiens netrin receptor Unc5h1, mRNA (cDNA clone IMAGE:5166762), containing frame-shift errors.

ACCESSION BC033727

VERSION BC033727.1 GI:21707230

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1532)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12477932

REFERENCE 2 (bases 1 to 1532)

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (02-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc\\_mgc@nhgri.nih.gov](mailto:nisc_mgc@nhgri.nih.gov)  
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 68 Row: i Column: 2  
This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction  
This clone has the following problem: frame shifted.

FEATURES

source 1. .1532  
/organism="Homo sapiens"  
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/clone\_lib="NIH\_MGC\_119"  
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/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 26.8%; Score 736.6; DB 11; Length 1532;  
Best Local Similarity 84.2%; Pred. No. 1.5e-115;  
Matches 917; Conservative 0; Mismatches 4; Indels 168; Gaps 1;

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Qy      637 GTATACATCACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCC 696
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Qy      697 AACTACACCTGCGTGGCCAAGAACATCGTGGCACGTCGCCGAGCGCCTCCGCTGCTGTC 756
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Qy      757 ATCGTCTACGTGAACGGTGGGTGGTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGC 816
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Db     1032 ATCGTCTACGTG----- 1043

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 Db 1524 CCCCTGGGT 1532

# RESULT 10

AI951556

LOCUS AI951556 788 bp mRNA linear EST 09-MAR-2000  
 DEFINITION wv36f04.x1 NCI\_CGAP\_Ov18 Homo sapiens cDNA clone IMAGE:2531647 3' similar to TR:008721 008721 TRANSMEMBRANE RECEPTOR UNC5H1. ;, mRNA sequence.

ACCESSION

AI951556

VERSION

AI951556.1 GI:5743866

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 788)

AUTHORS

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Insert Length: 1125 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 446.

FEATURES  
source Location/Qualifiers  
1. .788  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2531647"  
/tissue\_type="fibrotheoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NCI\_CGAP\_Ov18"  
/note="Organ: ovary; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGACATTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "

#### ORIGIN

Query Match 26.7%; Score 735.2; DB 9; Length 788;  
Best Local Similarity 96.5%; Pred. No. 1.9e-115;  
Matches 749; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

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Qy      1469 CCGAGGAGTTCGTCTCCCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCA 1528
          |||
Db        1 CCGAGGAGTTCGTCTCCCGCCTCTCCGCCAGAACTACTTCCGCTCCCTGCCCCGAGGCA 60

Qy      1529 CCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATA 1588
          |||
Db        61 CCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATA 120

Qy      1589 CAGGTATCAGCCTCCTCATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATCT 1648
          |||
Db       121 CAGGAATCAGCCTCCTCATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATCT 180

Qy      1649 ACCTCACGCTGCACAAGCCGGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCCTGC 1708
          |||
Db       181 ACCTCACGCTGCACAAGCCGGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCCTGC 240

Qy      1709 TGAGTCCCATCGTTAGCTGTGGACCCCTGGCGTCTGCTCACC CGCCAGTCATCCTGG 1768
          |||
Db       241 TGAGTCCCATCGTTAGCTGTGGACCCCTGGCGTCTGCTCACC CGCCAGTCATCCTGG 300

Qy      1769 CTATGGACCACTGTGGGGAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGT 1828
          |||
Db       301 CTATGGACCACTGTGGGGAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGT 360

Qy      1829 CGTGCGAGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCT 1888
          |||
Db       361 CGTGCGAGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCT 420

Qy      1889 ACTACTGCCAGCTGGAGGCCAGTGCCCTGCTACGTCTTCACCGAGCAGCTGGGCGCGCTTTG 1948
          |||
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Db 421 ACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGAGCCGCTATG 480  
 Qy 1949 CCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTG 2008  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 481 CCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTG 540  
 Qy 2009 CGCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCC 2068  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 541 CGCCGGTGGCCTGCACCTCCCTCGAGTACAACATACTGGTCTACTGCCTGCATGACACTC 600  
 Qy 2069 ACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGG 2128  
 ||||||||||||| | ||||||||||||||||||||||| ||||||||||||||||  
 Db 601 ACGATGCACTCAACGTAGTGGTGCAGCTGGAGAAGCAGCTGCAGGGACAGCTGATCCAGG 660  
 Qy 2129 AGCCACGGGTCCTGCACCTTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATG 2188  
 ||||| ||| ||||||||||||||||||||||||||||||||||||||| |||||||||  
 Db 661 AGCCACTGGTACTGCACCTTCAAGGACAGTTACCACAACCTGCGCCTATNCATCCACGATG 720  
 Qy 2189 TGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTT 2244  
 ||||||||| || | ||||||||| ||||||||||| ||||||| || |  
 Db 721 TGCCCAGCTNCCNTGTGGAGAGTAAGCTTCTTGTCAGCTACCCAGAGATCCNCTAT 776

RESULT 11  
 BX348193/c

LOCUS BX348193 843 bp mRNA linear EST 05-MAY-2003  
 DEFINITION BX348193 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens  
 cDNA clone CS0DB008YE02 5-PRIME, mRNA sequence.

ACCESSION BX348193

VERSION BX348193.1 GI:30367258

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 843)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 3239.r For  
 more information about this cluster, see

<http://www.genoscope.cns.fr/>

[cgi-bin/cluster.cgi?seq=CS0BAF004ZD01\\_AF00293\\_1&cluster=3239.r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BAF004ZD01_AF00293_1&cluster=3239.r).

Contact : Feng Liang Email : [fliang@lifetech.com](mailto:fliang@lifetech.com) URL :

<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0BAF004ZD01\_AF00293\_1.

FEATURES

source

Location/Qualifiers

1. .843

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0DB008YE02"



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Db      165 CAGCACTAGTGACCTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAG 106
Qy      2370 CTTCAGCATCAACTTCAACATCACCAAGGACACAAGGTTTGGCTGAGCTGCTGGCTCTGGA 2429
|||||
Db      105 CTTCAGCATCAACTTCAACATCACCAAGGACACAAGGTTTGGCTGAGCTGCTGGCTCTGGA 46
Qy      2430 GAGTGAAGCGGGGGTCCCAGCCCTGGTGGGCCCC 2463
|||||
Db      45 GAGTGAAGCGGGGGTCCCAGNCCCTGGTGGGCCC 12

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RESULT 12

BI818609

LOCUS BI818609 818 bp mRNA linear EST 04-OCT-2001

DEFINITION 603033362F1 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:5174559 5', mRNA sequence.

ACCESSION BI818609

VERSION BI818609.1 GI:15929902

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 818)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11434 row: 1 column: 16

High quality sequence stop: 744.

FEATURES

source

Location/Qualifiers

1. .818

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5174559"

/lab\_host="DH10B"

/clone\_lib="NIH\_MGC\_115"

/note="Organ: pooled brain, lung, testis; Vector:

pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA

source anonymous pool of 6 male brains, age range 23-27; 1

male lung, age 27; and 1 male testis, age 69. Library is

oligo-dT primed and directionally cloned (EcoRV site is

destroyed upon cloning). Average insert size 1.8 kb,

insert size range 1-3 kb. Library is normalized and

enriched for full-length clones and was constructed by C.

Gruber (Invitrogen). Research Genetics tracking code

021. Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 26.0%; Score 716.4; DB 12; Length 818;  
 Best Local Similarity 97.7%; Pred. No. 3.2e-112;  
 Matches 748; Conservative 0; Mismatches 16; Indels 2; Gaps 2;

Qy	43	GCCATGGCCGTCCGGCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGG	102
Db	1	GCCATGGCCGTCCGGCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGG	60
Qy	103	CTCCGCGGCTCGGGTGCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCCTGGTGCCAAC	162
Db	61	CTCCGCGGCTCGGGTGCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCCTGGTGCCAAC	120
Qy	163	CCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCAGGATGTGTACATCGTCAAGAACAAG	222
Db	121	CCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCAGGATGTGTACATCGTCAAGAACAAG	180
Qy	223	CCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTCAAGTGCAACGGG	282
Db	181	CCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTCAAGTGCAACGGG	240
Qy	283	GAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTG	342
Db	241	GAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTG	300
Qy	343	CCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTTCGGGCTG	402
Db	301	CCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTTCGGGCTG	360
Qy	403	GAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAG	462
Db	361	GAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAG	420
Qy	463	GCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAG	522
Db	421	GCCTACATCCGCATAGCCTATTTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAG	480
Qy	523	GTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCC	582
Db	481	GTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCC	540
Qy	583	GAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATAC	642
Db	541	GAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATAC	600
Qy	643	ATCACGCGGGAGCACAGCCTGGTGGTGCACAGGCCCGCCTTGCTGACACGGCCAACCTAC	702
Db	601	ATCACGCGGGAGCACAGCCTGGTGGTGCACAGGCCCGCCTTGCTGACACGGCCAACCTAC	660
Qy	703	ACCTGCGTGGCCAAGAACATCGTGGCACGTC-GCCGCAGCGCCTCCGCTGCTGTCATCGT	761
Db	661	ACCTGCGTGGCCAAGAACATCGTGGCACGTCAGCCGCAGGGCCTCCGCTGCTGTCATCGT	720
Qy	762	CTACGTGAACGGTGGGTGGTTCGACG-TGGACCGAGTGGTCCGTCTG	806
Db	721	CTACGTGGACGGCAGCTGGAGCCCGTTGGAGCCAGTGGTCCGGGCTG	766

RESULT 13

BX364574

LOCUS BX364574 909 bp mRNA linear EST 05-MAY-2003

DEFINITION BX364574 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DC023YB10 5-PRIME, mRNA sequence.

ACCESSION BX364574

VERSION BX364574.1 GI:30368812

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 909)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 3529.f For more information about this cluster, see

<http://www.genoscope.cns.fr/>

[cgi-bin/cluster.cgi?seq=CS1AC006ZF06QP1&cluster=3529.f](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS1AC006ZF06QP1&cluster=3529.f). Contact :

Feng Liang Email : [fliang@lifetech.com](mailto:fliang@lifetech.com) URL :

<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS1AC006ZF06QP1.

FEATURES

source

Location/Qualifiers

1. .909

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0DC023YB10"

/tissue\_type="NEUROBLASTOMA COT 25-NORMALIZED"

/clone\_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 25.1%; Score 692; DB 13; Length 909;

Best Local Similarity 99.0%; Pred. No. 5.1e-108;

Matches 703; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

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Qy      1 CCGCGGGGCCCCGCGCCCGGGCCCGCCGCGCTGCCCGCCCGCGGCCATGGCCGTCCGGCCC 60
          ||||:|||||
Db      201 CCGCRGGGCCCCGCGCCCGGGCCCGCCGCGCTGCCCGCCCGCGGCCATGGCCGTCCGGCCC 260

Qy      61 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 120
          |||||
Db      261 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 320

Qy      121 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 180

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      |||:|||||
Db      321 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCYAACCCGGACCTGCTTCCCCAC 380
Qy      181 TTCCTGGTGGAGCCCAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240
      |||
Db      381 TTCCTGGTGGAGCCCAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 440
Qy      241 AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCCCCAGGTG 300
      |||
Db      441 AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCCCCAGGTG 500
Qy      301 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGC 360
      |||:|||||
Db      501 GACCACGTGATCGAGCGCA-SACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGC 559
Qy      361 ATTAATGTCTCAAGGCAGCAGGTTCGAGAAGGTGTTTCGGGCTGGAGGAATACTGGTGCCAG 420
      |||
Db      560 ATTAATGTCTCAAGGCAGCAGGTTCGAGAAGGTGTTTCGGGCTGGAGGAATACTGGTGCCAG 619
Qy      421 TGCCTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 480
      |||
Db      620 TGCCTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 679
Qy      481 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 540
      |||
Db      680 TATTTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 739
Qy      541 ATCGTGCTGCCCTGCCGTCCACCGAGGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600
      |||
Db      740 ATCGTGCTGCCCTGCCGTCCACCGAGGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 799
Qy      601 AACGAGGACCTGGTGGACCCGCTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 660
      |||
Db      800 AACGAGGACCTGGTGGACCCGCTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 859
Qy      661 CTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGT 710
      |||
Db      860 CTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGT 909

```

#### RESULT 14

AY411748

LOCUS AY411748 2532 bp DNA linear GSS 12-DEC-2003

DEFINITION Pan troglodytes HCM4327 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY411748

VERSION AY411748.1 GI:39767716

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 2532)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 2532)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers  
source 1. .2532  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
gene <1..>2532  
/locus\_tag="HCM4327"

ORIGIN

Query Match 24.6%; Score 678.2; DB 29; Length 2532;  
Best Local Similarity 54.4%; Pred. No. 1.9e-105;  
Matches 1370; Conservative 0; Mismatches 1021; Indels 129; Gaps 9;

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Qy      352 GAGGTCCGCATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTCTGGGCTGGAGGAATAC 411
        ||||| |  ||  | || ||  ||||| ||||| ||| || | || ||||| ||||| |||
Db      13  GAGGTGCAGATCGAGGTGTGCGGGCAGCAGGTGGAGGAGCTCTTTGGGCTGGAGGATTAC 72

Qy      412 TGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATC 471
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Db      73  TGGTGCCAGTGCGTGGCCTGGAGCTCTGCGGGCACCACCAAGAGTCGCCGAGCCTACGTC 132

Qy      472 CGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTG 531
        ||||| |||
Db      133 CGCATCGCCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 192

Qy      532 GAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAG 591
        |||||
Db      193 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTGGAA 252

Qy      592 TGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGG 651
        ||||| ||| ||||| | | ||||| ||| ||||| |||| | |||||
Db      253 TGGCTCAAGAATGAGGATGTCATCGACCCACCCAGGACACCAACTTCCTGCTCACCATC 312

Qy      652 GAGCACAGCCTGGTGGTGGGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGTG 711
        || ||||| ||| | | || ||||| ||||| ||||| ||||| ||||| |||||
Db      313 GACCACAACCTCATCATCCGCCAGGCCCGCCTGTGCGACACTGCCAACTATACCTGCGTG 372

Qy      712 GCCAAGAACATCGTGGCACGTCGCCGAGCGCCTCCGCTGCTGTCATCGTCTACGTGAAC 771
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      373 GCCAAGAACATCGTGGCCAAACGCCGGAGCACCAGTCCACCGTCATCGTCTACGTGAAT 432

Qy      772 GGTGGGTGGTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGG 831
        || || ||||| | ||| | ||||| |||| | | ||||| | |||||
```

Db	433	GGCGGCTGGTCCAGCTGGGCAGAGTGGTCGCCCTGCTCCAACCGCTGTGGNNGANNCTGG	492
Qy	832	CAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAG	891
Db	493	CAGAAGCGCACCCGGACCTGCACCAACCCGCCCCACTCAACGGAGGGNNNTCTGCGAG	552
Qy	892	GGCAGAAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCAGTAGACGGCAGCTGGAGC	951
Db	553	GGCCANNTCGATGGGGCGTGGACG	612
Qy	952	CCGTGGAGCAAGTGGTGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGC	1011
Db	613	GAGTGGAGCAAGTGGTCAAGCTGCAGCACTGAGTGTGCCCACTGGCGTAGCCGCGAGTGC	672
Qy	1012	TCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGC	1071
Db	673	ATGGCGCCCCACCCAGAACGGAGGCCGTGACTGCAGCGGGACGCTGCTCGACTCTAAG	732
Qy	1072	AACTGTACCAGTGACCTCTGTGTACACAGTGCTTCT-----	1107
Db	733	AACTGCACAGATGGGCTGTGCATGCAAAATAAGAAAACCTCTAAGCGACCCCAACAGCCAC	792
Qy	1108	-----GGCCCTGAGGACGTGGCCCTCTATGTGGGCCTC---ATCGCCGTGGCCGTC	1155
Db	793	CTGCTGGAGGCCTCAGGGGATGCGGCGCTGTATGCGGGGCTCGTGGTGGCCGTCTTCNTG	852
Qy	1156	TGCCTGGTCCCTGCTGCTGCTTGTCTCATCCTCGTTTATTGCCGAAGAAGGAGGGGCTG	1215
Db	853	GTCNTGGCAATCCTCATGGCGGTGGGGGTGGTGGTGTACCGCCGCAACTGCCGTGACTTC	912
Qy	1216	GACTCAGATGTGGCTGACTCGTCCATT---CTCACCTCAGGCTTCCAGCCCGTCAGCATC	1272
Db	913	GACACAGACATCACTGACTCATCTGCTGCCCTGACTGGTGGTTTCCACCCCGTCAACTTT	972
Qy	1273	AAGCCCAGCAAAGCAGACAACCCCATCTGCT-----CACCATCCAGCCGGACCTCAGC	1326
Db	973	AAGACGGCAAGGCCAGCAACCCGCAGTCTCTACACCCCTCTGTGCCTCCTGACCTGACA	1032
Qy	1327	ACCACCACCACCACTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGG-----	1374
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# RESULT 15

BF311804

LOCUS BF311804 934 bp mRNA linear EST 21-NOV-2000

DEFINITION 601897316F1 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:4126706 5', mRNA sequence.

ACCESSION BF311804

VERSION BF311804.1 GI:11259566

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 934)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [image.llnl.gov](http://image.llnl.gov)

Plate: LLCM1016 row: p column: 03

High quality sequence stop: 707.

FEATURES Location/Qualifiers

source 1. .934

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4126706"

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/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_19"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

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# ORIGIN

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Query Match          24.4%; Score 672.6; DB 10; Length 934;
Best Local Similarity 93.3%; Pred. No. 1.1e-104;
Matches 747; Conservative 0; Mismatches 49; Indels 5; Gaps 4;

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Qy      1596 CAGCCTCCTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCAC 1655
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Qy      1656 GCTGCACAAGCCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCC 1715
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Qy	1716	CATCGTTAGCTGTGGACCCCCCTGGCGTCTGCTCACCCGGCCAGTCATCC--TGGCTATG	1773
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Qy	1834	GAGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTAC	1893
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Qy	1894	TGCCAGCTGGAGGCCAGTGCC	1914
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Job time : 6771 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2004, 09:28:21 ; Search time 10430 Seconds  
(without alignments)  
11436.244 Million cell updates/sec

Title: US-10-624-932-1  
Perfect score: 2752  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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12: gb\_sy:\*  
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 38: em\_sy:\*  
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Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

#### SUMMARIES

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6	2259	82.1	3014	6	BD057524	BD057524 Netrin re	
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# ALIGNMENTS

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LOCUS AX449572 2752 bp DNA linear PAT 03-JUL-2002

DEFINITION Sequence 1 from Patent WO0210216.

ACCESSION AX449572

VERSION AX449572.1 GI:21698195

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Padigaru,M., Mezes,P., Mishra,V., Burgess,C., Casman,S., Grosse,W.M., Alsobrook,J.P., Lepley,D.M., Gerlach,V.L., Macdougall,J.R. and Smithson,G.

TITLE Proteins and nucleic acids encoding same

JOURNAL Patent: WO 0210216-A 1 07-FEB-2002; Curagen Corporation (US)

FEATURES Location/Qualifiers

source 1. .2752

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/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 2752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1381	CCCAAGTTCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACACA	1440
Qy	1441	CTGACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCTCTCCACCCAG	1500
Db	1441	CTGACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCTCTCCACCCAG	1500
Qy	1501	AACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTC	1560
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Db	1561	CTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCC	1620
Qy	1621	ATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGG	1680
Db	1621	ATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGG	1680
Qy	1681	TTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCTGGC	1740
Db	1681	TTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCTGGC	1740
Qy	1741	GTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGAC	1800
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Qy	1921		GTCTTCACCGAGCAGCTGGGCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCC	1980
Db	1921		GTCTTCACCGAGCAGCTGGGCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCC	1980
Qy	1981		GCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAAC	2040
Db	1981		GCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAAC	2040
Qy	2041		ATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAG	2100
Db	2041		ATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAG	2100
Qy	2101		AAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGACAGTTAC	2160
Db	2101		AAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGACAGTTAC	2160
Qy	2161		CACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGGAAGAGTAAGCTCCTT	2220
Db	2161		CACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGGAAGAGTAAGCTCCTT	2220
Qy	2221		GTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCAC	2280
Db	2221		GTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCAC	2280
Qy	2281		TGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGG	2340
Db	2281		TGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGG	2340
Qy	2341		GTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAGGAC	2400
Db	2341		GTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAGGAC	2400
Qy	2401		ACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGTCCCAGCCCTGGTGGGC	2460
Db	2401		ACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGTCCCAGCCCTGGTGGGC	2460
Qy	2461		CCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGACCCA	2520
Db	2461		CCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGACCCA	2520
Qy	2521		CCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAGCCAT	2580
Db	2521		CCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAGCCAT	2580
Qy	2581		CTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCG	2640
Db	2581		CTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCG	2640
Qy	2641		CGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAG	2700
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AX451652  
LOCUS AX451652 2697 bp DNA linear PAT 03-JUL-2002  
DEFINITION Sequence 1 from Patent WO0233080.  
ACCESSION AX451652  
VERSION AX451652.1 GI:21698587  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Koehler, R.H.  
TITLE Regulation of human netrin binding membrane receptor unc5h-1  
JOURNAL Patent: WO 0233080-A 1 25-APR-2002;  
Bayer Aktiengesellschaft (DE)  
FEATURES Location/Qualifiers  
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ORIGIN

Query Match 97.7%; Score 2687.4; DB 6; Length 2697;  
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Qy     106 CGCGGCTCGGGTGCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCG 165
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Db     61 CGCGGCTCGGGTGCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCG 120

Qy     166 GACCTGCTTCCCCACTTCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCA 225
          |||
Db     121 GACCTGCTTCCCCACTTCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCA 180

Qy     226 GTGCTGCTTGTGTGCAAGGCCGTGCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAG 285
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Db     181 GTGCTGCTTGTGTGCAAGGCCGTGCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAG 240

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Qy     346 ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTCTGGGCTGGAG 405
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Db     301 ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTCTGGGCTGGAG 360

Qy     406 GAATACTGGTGCCAGTGCGTGGCATGGAGCTCTCGGGCACCACCAAGAGTCAGAAGGCC 465
          |||
Db     361 GAATACTGGTGCCAGTGCGTGGCATGGAGCTCTCGGGCACCACCAAGAGTCAGAAGGCC 420
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Qy	466	TACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG	525
Db	421	TACATCCGCATAGCCTATTTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG	480
Qy	526	TCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAG	585
Db	481	TCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAG	540
Qy	586	GTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATC	645
Db	541	GTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATC	600
Qy	646	ACGCGGGAGCACAGCCTGGTGGTGCACAGGCCCGCCTTGCTGACACGGCCAACCTACACC	705
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Qy	706	TGCGTGGCCAAGAACATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTCTAC	765
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Qy	766	GTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGC	825
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Qy	826	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTC	885
Db	781	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTC	840
Qy	886	TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGC	945
Db	841	TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGC	900
Qy	946	TGGAGCCCCTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGT	1005
Db	901	TGGAGCCCCTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGT	960
Qy	1006	GAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGAC	1065
Db	961	GAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGAC	1020
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Qy	1186	CTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTC	1245
Db	1141	CTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTC	1200
Qy	1246	ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTC	1305
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Qy	1306	ACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG	1365
Db	1261	ACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG	1320
Qy	1366	CAGGATGGGCCCAGCCCCAAGTTCCAGCTACCAATGGGCACCTGCTCAGCCCCCTGGGT	1425
Db	1321	CAGGATGGGCCCAGCCCCAAGTTCCAGCTACCAATGGGCACCTGCTCAGCCCCCTGGGT	1380
Qy	1426	GGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCC	1485
Db	1381	GGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCC	1440
Qy	1486	CGCCTCTCCACCCAGAATACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTAT	1545
Db	1441	CGCCTCTCCACCCAGAATACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTAT	1500
Qy	1546	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTC	1605
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Qy	1606	ATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG	1665
Db	1561	ATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG	1620
Qy	1666	CCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGC	1725
Db	1621	CCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGC	1680
Qy	1726	TGTGGACCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGG	1785
Db	1681	TGTGGACCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGG	1740
Qy	1786	GAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG	1845
Db	1741	GAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG	1800
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Db	1801	GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAG	1860
Qy	1906	GCCAGTGCCTGTACGTCTTACCCAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCC	1965
Db	1861	GCCAGTGCCTGTACGTCTTACCCAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCC	1920
Qy	1966	CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC	2025
Db	1921	CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC	1980
Qy	2026	TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG	2085
Db	1981	TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG	2040
Qy	2086	GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCAC	2145
Db	2041	GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCAC	2100
Qy	2146	TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGG	2205



Db	2101	TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGG	2160
Qy	2206	AAGAGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACG	2265
Db	2161	AAGAGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACG	2220
Qy	2266	CAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTG	2325
Db	2221	CAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTG	2280
Qy	2326	GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTC	2385
Db	2281	GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTC	2340
Qy	2386	AACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTC	2445
Db	2341	AACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTC	2400
Qy	2446	CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATT	2505
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Qy	2506	TCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTC	2565
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Db	2521	CACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTC	2580
Qy	2626	AACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTG	2685
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Qy	2686	GCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTGCGGAGGCTGAGTGCTGA	2742
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 DEFINITION Sequence 1 from Patent WO0229038.  
 ACCESSION AX527916  
 VERSION AX527916.1 GI:25172359  
 KEYWORDS .  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Herrmann,J.L., Rastelli,L. and Shimkets,R.A.  
 TITLE Novel proteins and nucleic acids encoding same and antibodies  
 directed against these proteins  
 JOURNAL Patent: WO 0229038-A 1 11-APR-2002;  
 Curagen Corporation (US)

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FEATURES                      Location/Qualifiers
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ORIGIN

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Query Match          97.3%;  Score 2676.4;  DB 6;  Length 2881;
Best Local Similarity 98.9%;  Pred. No. 0;
Matches 2728;  Conservative 0;  Mismatches 21;  Indels 9;  Gaps 3;

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Qy     61  GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 120
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Qy    121  CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 180
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Qy    181  TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240
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Qy    241  AAGGCCGTGCCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 300
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Db	762	ATCGTGGCACGTGCGCCGAGCGCCTCCGCTGCTGTTCATCGTCTACGTGAACGGTGGGTGG	821
Qy	781	TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG	840
Db	822	TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG	881
Qy	841	AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTCTGTGAGGGGCAGAAT	900
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Qy	901	GTCCAGAA---AACAGCCTGCGCCACCCTGTGCCAGTAGACGGCAGCTGGAGCCCGTGG	957
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Qy	958	AGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGAC	1017
Db	1002	AGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGAC	1061
Qy	1018	CCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGT	1077
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Qy	1198	CGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTC	1257
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Qy	1318	GACCTCAGCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCC	1377
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Qy	1378	AGCCCCAAGTTCAGCTCACCATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCAC	1437
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Qy	1438	ACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACC	1497
Db	1479	ACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACC	1538
Qy	1498	CAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAAC	1557
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Qy	1558	TTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGAT	1617
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Qy	1618	GCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTG	1677
Db	1659	GCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTG	1718
Qy	1678	AGGTTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCT	1737
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Qy	1738	GGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCT	1797
Db	1779	GGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCT	1838
Qy	1798	GACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGG---AGGATGTG	1854
Db	1839	GACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGCAGGATGTG	1898
Qy	1855	CTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCC	1914
Db	1899	CTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCC	1958
Qy	1915	TGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTG	1974
Db	1959	TGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTG	2018
Qy	1975	GCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAG	2034
Db	2019	GCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAG	2078
Qy	2035	TACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAG	2094
Db	2079	TACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAG	2138
Qy	2095	CTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGAC	2154
Db	2139	CTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGAC	2198
Qy	2155	AGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGGAAGAGTAAG	2214
Db	2199	AGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGGAAGAGTAAG	2258
Qy	2215	CTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTAC	2274
Db	2259	CTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTAC	2318
Qy	2275	TTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAG	2334
Db	2319	TTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAG	2378
Qy	2335	CTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACC	2394
Db	2379	CTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACC	2438

Qy	2395	AAGGACACAAGGTTTGGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTG	2454
Db	2439	AAGGACACAAGGTTTGGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTG	2498
Qy	2455	GTGGGCCCCAGTGCCTTCAAGATCCCCTTCTCATTCCGGCAGAAGATAATTTCCAGCCTG	2514
Db	2499	GTGGGCCCCAGTGCCTTCAAGATCCCCTTCTCATTCCGGCAGAAGATAATTTCCAGCCTG	2558
Qy	2515	GACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGAC	2574
Db	2559	GACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGAC	2618
Qy	2575	AGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGG	2634
Db	2619	AGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGG	2678
Qy	2635	GAGGCGCGGCACCTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTG	2694
Db	2679	GAGGCGCGGCACCTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTG	2738
Qy	2695	GGCCAGCCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGAGGCCGGCCAG	2752
Db	2739	GGCCAGCCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGAGGCCGGCCAG	2796

✓**RESULT 4**  
**AX367094**  
**LOCUS** AX367094 3580 bp DNA linear PAT 16-FEB-2002  
**DEFINITION** Sequence 13 from Patent WO0198354.  
**ACCESSION** AX367094  
**VERSION** AX367094.1 GI:18855296  
**KEYWORDS** .  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE** 1  
**AUTHORS** Griffin,J.A., Kallick,D.A., Tribouley,C.M., Yue,H., Nguyen,D.B.,  
Tang,Y.T., Lal,P., Policky,J.L., Azimzai,Y., Lu,D.A., Graul,R.,  
Yao,M.G., Burford,N., Hafalia,A.J., Baughn,M.R., Bandman,O.,  
Patterson,C., Yang,J., Xu,Y., Warren,B.A., Ding,L. and  
Sanjanwala,M.S.  
**TITLE** Receptors  
**JOURNAL** Patent: WO 0198354-A 13 27-DEC-2001;  
Incyte Genomics, Inc. (US)  
**FEATURES** Location/Qualifiers  
source 1. .3580  
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/note="Incyte ID No: 6052371CB1"  
**ORIGIN**  
  
Query Match 85.6%; Score 2356; DB 6; Length 3580;  
Best Local Similarity 93.6%; Pred. No. 0;  
Matches 2537; Conservative 0; Mismatches 5; Indels 168; Gaps 1;

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Qy 103 CTCCGCGGCTCGGGTGCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAAC 162  
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 Db 61 CTCCGCGGCTCGGGTGCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAAC 120

Qy 163 CCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCAGGATGTGTACATCGTCAAGAACAAG 222  
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 Db 121 CCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCAGGATGTGTACATCGTCAAGAACAAG 180

Qy 223 CCAGTGCTGCTTGTGTGCAAGGCCGTGCCGCCACGCAGATCTTCTTCAAGTGCAACGGG 282  
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 Db 181 CCAGTGCTGCTTGTGTGCAAGGCCGTGCCGCCACGCAGATCTTCTTCAAGTGCAACGGG 240

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 Db 301 CCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTCCGGGCTG 360

Qy 403 GAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAG 462  
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 Db 361 GAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAG 420

Qy 463 GCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAG 522  
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 Db 721 TACGTG----- 726

Qy 823 CGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCT 882  
 Db 727 ----- 726

Qy 883 TTCTGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCAGTAGACGGC 942



Db	727	-----		GACGGC	732
Qy	943	AGCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGC	1002		
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Qy	1003	CGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTG	1062		
Db	793	CGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTG	852		
Qy	1063	GACACCCGCAACTGTACCACTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTG	1122		
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Qy	1123	GCCCTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGTCTCCTC	1182		
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Qy	1183	ATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATT	1242		
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Qy	1243	CTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTG	1302		
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Qy	1303	CTCACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCC	1362		
Db	1093	CTCACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCC	1152		
Qy	1363	CGGCAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTG	1422		
Db	1153	CGGCAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTG	1212		
Qy	1423	GGTGGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTC	1482		
Db	1213	GGTGGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTC	1272		
Qy	1483	TCCCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACC	1542		
Db	1273	TCCCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACC	1332		
Qy	1543	TATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTC	1602		
Db	1333	TATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGAATCAGCCTC	1392		
Qy	1603	CTCATCCCCCAGATGCCATAACCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCAC	1662		
Db	1393	CTCATCCCCCAGATGCCATAACCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCAC	1452		
Qy	1663	AAGCCGGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTT	1722		
Db	1453	AAGCCGGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTT	1512		
Qy	1723	AGCTGTGGACCCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGT	1782		

Db	1513	AGCTGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGT	1572
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Qy	1843	TGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTG	1902
Db	1633	TGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTG	1692
Qy	1903	GAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAG	1962
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Qy	1963	GCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGC	2022
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Qy	2023	ACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAG	2082
Db	1813	ACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAG	1872
Qy	2083	GAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTTG	2142
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Qy	2143	CACTTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTG	2202
Db	1933	CACTTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTG	1992
Qy	2203	TGGAAGAGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGC	2262
Db	1993	TGGAAGAGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGC	2052
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Db	2053	ACGCAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGAC	2112
Qy	2323	CTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAAC	2382
Db	2113	CTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAAC	2172
Qy	2383	TTCAACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGG	2442
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Qy	2503	ATTTCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAA	2562
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# RESULT 5

MMU487852

LOCUS MMU487852 3992 bp mRNA linear ROD 24-SEP-2002

DEFINITION Mus musculus mRNA for netrin receptor Unc5h1 (Unc5h1 gene).

ACCESSION AJ487852

VERSION AJ487852.1 GI:22035783

KEYWORDS netrin receptor Unc5h1; Unc5h1 gene.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE 1

AUTHORS Engelkamp,D.

TITLE Cloning of three mouse Unc5 genes and their expression patterns at  
 mid-gestation

JOURNAL Mech. Dev. 118 (1-2), 191-197 (2002)

MEDLINE 22239710

PUBMED 12351186

## REFERENCE 2 (bases 1 to 3992)

AUTHORS Engelkamp,D.

TITLE Direct Submission

JOURNAL Submitted (15-MAY-2002) Neuroanatomy, Max Planck Institute for  
 Brain Research, Deutschordenstrasse 46, Frankfurt 60528, GERMANY

## FEATURES Location/Qualifiers

source

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Db	1867	TTGCCCCTAGCTGGCTGTCAGACCTGCTGAGTCCATCGTTAGCTGTGGGCCCCCAGGA	1926
Qy	1741	GTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGAC	1800
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Qy	1801	AGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCAC	1860
Db	1987	AGCTGGAGCCTGCGCCTCAAAAAGCAGTCCTGTGAGGGCAGCTGGGAGGACGTGCTGCAC	2046
Qy	1861	CTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTAC	1920
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Qy	2041	ATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAG	2100
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Db	2347	CACAACCTACGTCTGTCCATCCACGACGTGCCCAGCTCCCTGTGGAAGAGCAAGCTCCTT	2406
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Db	2407	GTCAGCTACCAGGAGATCCCCTTTTACCACATCTGGAATGGCACTCAGCAGTATCTGCAC	2466
Qy	2281	TGCACCTTCACCCTGGAGCGTGTGACCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGG	2340

Db 2467 TGCACCTTCACCCTGGAGCGCGTCAATGCCAGCACCAGCGACCTGGCCTGCAAGGTGTGG 2526

Qy 2341 GTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAGGAC 2400  
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Db 2527 GTGTGGCAGGTGGAGGGAGATGGACAGAGCTTCAACATCAACTTTAACATCACTAAGGAC 2586

Qy 2401 ACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGC 2460  
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Db 2587 ACGAGGTTTGCTGAAATGCTGGCTCTGGAGAGTGAAGGGGGGTCCCAGCCCTGGTGGGC 2646

Qy 2461 CCCAGTGCCTTCAAGATCCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGACCCA 2520  
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Qy 2521 CCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAGCCAT 2580  
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Qy 2581 CTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCG 2640  
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Db 2827 CGGCAC'TCCCCAACGGCAACCTCGGCCAGCTGGCCGCAGCTGTGGCCGGACTGGGCCAG 2886

Qy 2701 CCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGTCTGAGGCCGGCCAG 2752  
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Db 2887 CCAGATGCTGGCCTCTTCACCGTGTCTAGAGGCCGAGTGTCTGAGACCAGCCAG 2938

# RESULT 6

BD057524

LOCUS BD057524 3014 bp DNA linear PAT 27-AUG-2002

DEFINITION Netrin receptors.

ACCESSION BD057524

VERSION BD057524.1 GI:22603130

KEYWORDS JP 2001505062-A/1.

SOURCE synthetic construct

ORGANISM synthetic construct  
 artificial sequences.

REFERENCE 1 (bases 1 to 3014)

AUTHORS Lavigne,M.T., Leonardo,D.E., Hinck,L., Masu,M. and Masu,K.K.

TITLE Netrin receptors

JOURNAL Patent: JP 2001505062-A 1 17-APR-2001;

THE REGENTS OF THE UNIV OF CALIFORNIA

COMMENT PN JP 2001505062-A/1

PD 17-APR-2001

PF 19-FEB-1998 JP 1998536840

PR 19-FEB-1997 US 08/808982

PI MARC TESSIER LAVIGNE,DAVID E LEONARDO,LINDSAY HINCK,MASAYUKI

PI MASU,

PI KAZUKO KEINO MASU

PC C07K1/00,C07K14/00,C07K17/00,C07H21/02,C07H21/04,G01N33/53 CC

Strandedness: Double;

CC Topology: Linear;

FH Key Location/Qualifiers.

FEATURES                      Location/Qualifiers  
       source                    1. .3014  
                               /organism="synthetic construct"  
                               /mol\_type="genomic DNA"  
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ORIGIN

Query Match                      82.1%;    Score 2259;    DB 6;    Length 3014;  
 Best Local Similarity    89.7%;    Pred. No. 0;  
 Matches 2427;    Conservative    0;    Mismatches    280;    Indels    0;    Gaps    0;

Qy	46	ATGGCCGTCCGGCCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTC	105
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Qy	106	CGCGGCTCGGGTGCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCG	165
Db	61	CGTGGTTCGGGTGCCAGCAGAGTGCCACGGTGGCCAATCCAGTGCCCGGTGCCAACCCC	120
Qy	166	GACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCA	225
Db	121	GACCTGCTGCCCCACTTCCTGGTAGAGCCTGAGGACGTGTACATTGTCAAGAACAAGCCG	180
Qy	226	GTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAG	285
Db	181	GTGTTGTTGGTGTGCAAGGCTGTGCCTGCCACCCAGATCTTCTTCAAGTGCAATGGGGAA	240
Qy	286	TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCC	345
Db	241	TGGGTCCGCCAGGTGATCACGTAATTGAACGCAGCACCGACAGCAGCAGCGGATTGCCA	300
Qy	346	ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTGCGGCTGGAG	405
Db	301	ACCATGGAGGTCCGTATCAACGTATCGAGGCAGCAGGTAGAGAAAGTGTGTTGGGCTGGAG	360
Qy	406	GAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC	465
Db	361	GAATACTGGTGCCAGTGTGTGGCATGGAGCTCCTCGGGTACCACCAAAAGTCAGAAGGCC	420
Qy	466	TACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG	525
Db	421	TACATCCGGATTGCCTATTTGCGCAAGAACTTTGAGCAGGAGCCACTGGCCAAGGAAGTG	480
Qy	526	TCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAG	585
Db	481	TCACTGGAGCAAGGCATTGTACTACCTTGTCGCCCCCAGAAGGAATCCCCCAGCTGAG	540
Qy	586	GTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATC	645
Db	541	GTGGAGTGGCTTCGAAATGAGGACCTCGTGGACCCCTCCCTCGATCCCAATGTGTACATC	600
Qy	646	ACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCCGCCTTGCTGACACGGCCAACTACACC	705
Db	601	ACGCGGGAGCACAGCCTAGTCGTGCGTCAGGCCCCGCCTGGCCGACACGGCCAACTACACC	660
Qy	706	TGCGTGGCCAAGAATCATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCTATCGTCTAC	765

Db 661 TGTGTGGCCAAGAACATCGTAGCCCGTCGCCGAAGCACCTCTGCAGCGGTTCATTGTTTAT 720  
 Qy 766 GTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGC 825  
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 Db 721 GTGAACGGTGGGTGGTTCGACGTGGACTGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGT 780  
 Qy 826 GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTC 885  
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 Db 781 GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCACCTCTCAACGGGGGCGCCTTC 840  
 Qy 886 TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCAGTAGACGGCAGC 945  
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 Db 841 TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACTCTGTGCCAGTGGATGGGAGC 900  
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 Db 901 TGGAGTTCGTGGAGTAAGTGGTCAGCCTGTGGGCTTGACTGCACCCACTGGCGGAGCCGC 960  
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 Db 961 GAGTGCTCTGACCCAGCACCCCCGCAATGGAGGTGAGGAGTGTGCGGGTGCTGACCTGGAC 1020  
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 Qy 1246 ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTC 1305  
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 Db 1261 ACCATCCAGCCAGACCTCAGCACCAACCACCTACCACCTACCAGGGCAGTCTATGTTTCAGG 1320  
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 Qy 1426 GGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCC 1485  
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 Db 1381 AGTGGCCGCCATACGTTGCACCACAGCTCACCCACCTCTGAGGCTGAGGACTTCGTCTCC 1440  
 Qy 1486 CGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTAT 1545  
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 Db 1441 CGCCTCTCCACCCAAAATACTTTCGTTCCCTGCCCCGCGGCACCAGCAACATGGCCTAC 1500  
 Qy 1546 GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTC 1605  
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 Db 1501 GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACGGGGATCAGCCTCCTC 1560

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Db	1561	ATACCCCGGATGCCATCCCCGAGGAAAGATCTACGAGATCTACCTCACACTGCACAAG	1620
Qy	1666	CCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGC	1725
Db	1621	CCAGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCAGTCCGTTAGC	1680
Qy	1726	TGTGGACCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGG	1785
Db	1681	TGTGGGCCCCCAGGAGTCCTGCTCACCCGGCCAGTCATCCTTGCAATGGACCACTGTGGA	1740
Qy	1786	GAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG	1845
Db	1741	GAGCCCAGCCCTGACAGCTGGAGTCTGCGCCTCAAAAAGCAGTCCTGCGAGGGCAGTTGG	1800
Qy	1846	GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAG	1905
Db	1801	GAGGATGTGCTGCACCTTGGTGAGGAGTCACCTTCCACCTCTACTACTGCCAGCTGGAG	1860
Qy	1906	GCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCC	1965
Db	1861	GCCGGGGCCTGCTATGTCTTCACGGAGCAGCTGGGCCGCTTTGCCCTGGTAGGAGAGGCC	1920
Qy	1966	CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC	2025
Db	1921	CTCAGCGTGGCTGCCACCAAGCGCCTCAGGCTCCTTCTGTTTGCTCCCGTGGCCTGTACG	1980
Qy	2026	TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG	2085
Db	1981	TCCCTTGAGTACAACATCCGAGTGTACTGCCTACACGACACCCACGACGCTCTCAAGGAG	2040
Qy	2086	GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCAC	2145
Db	2041	GTGGTGCAGCTGGAGAAGCAGCTAGGTGGACAGCTGATCCAGGAGCCTCGCGTCCCTGCAC	2100
Qy	2146	TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGG	2205
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Qy	2206	AAGAGTAAGTCCCTTGTGCTAGCTACCAGGAGATCCCTTTTATCACATCTGGAATGGCACG	2265
Db	2161	AAGAGCAAGTACTTGTGCTAGCTACCAGGAGATCCCTTTTACCACATCTGGAACGGCACC	2220
Qy	2266	CAGCGGTACTTGCCTGCACCTTACCCTGGAGCGTGTGAGCCCGAGCTAGTGACCTG	2325
Db	2221	CAGCAGTATCTGCACTGCACCTTACCCTGGAGCGCATCAACGCCAGCACCAGCGACCTG	2280
Qy	2326	GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTC	2385
Db	2281	GCCTGCAAGGTGTGGGTGTGGCAGGTGGAGGGAGATGGGCAGAGCTTCAACATCAACTTC	2340
Qy	2386	AACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTC	2445
Db	2341	AACATCACTAAGGACACAAGGTTTGCTGAATTGTTGGCTCTGGAGAGTGAAGGGGGGGTC	2400



Qy 2446 CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATT 2505  
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 Db 2401 CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAAAAGATCATC 2460

Qy 2506 TCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAACTC 2565  
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 Db 2461 GCCAGTCTGGACCCACCCTGCAGCCGGGGCGCCGACTGGAGAACTCTAGCCCAGAAACTT 2520

Qy 2566 CACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTC 2625  
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 Db 2521 CACCTGGACAGCCATCTTAGCTTCTTTGCCTCCAAGCCCAGCCCTACAGCCATGATCCTC 2580

Qy 2626 AACCTGTGGGAGGCGCGGCACCTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTG 2685  
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 Db 2581 AACCTATGGGAGGCACGGCACCTTCCCCAACGGCAACCTCGGCCAGCTGGCAGCAGCTGTG 2640

Qy 2686 GCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCCGAGGCTGAGTGCTGAGGC 2745  
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 Db 2641 GCCGGACTGGGCCAACCAGATGCTGGCCTCTTCACGGTGTCCGAGGCCGAGTGTTGAGAC 2700

Qy 2746 CGGCCAG 2752  
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 Db 2701 CAGCCAG 2707

RESULT 7  
 AX268596

LOCUS AX268596 2697 bp DNA linear PAT 29-OCT-2001  
 DEFINITION Sequence 15 from Patent WO0175440.  
 ACCESSION AX268596  
 VERSION AX268596.1 GI:16541710  
 KEYWORDS .  
 SOURCE Rattus sp.  
 ORGANISM Rattus sp.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE 1  
 AUTHORS Cochran,S.W., Paterson,G.Y., Ohashi,Y.W., Morris,B.Y. and Pratt,J.Y.  
 TITLE Schizophrenia related genes  
 JOURNAL Patent: WO 0175440-A 15 11-OCT-2001;  
 WELFIDE CORPORATION (JP)

FEATURES Location/Qualifiers  
 source 1. .2697  
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ORIGIN

Query Match 81.8%; Score 2252.2; DB 6; Length 2697;  
 Best Local Similarity 89.7%; Pred. No. 0;  
 Matches 2419; Conservative 0; Mismatches 278; Indels 0; Gaps 0;

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Db	61	CGTGGTTCGGGTGCCAGCAGAGTGCCACGGTGGCCAATCCAGTGCCTGGTGCCAACCCG	120
Qy	166	GACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCA	225
Db	121	GACCTGCTGCCCCACTTCCTGGTAGAGCCTGAGGACGTGTACATTGTCAAGAACAAGCCG	180
Qy	226	GTGCTGCTTGTGTGCAAGGCCGTGCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAG	285
Db	181	GTGTTGTTGGTGTGCAAGGCTGTGCCTGCCACCCAGATCTTCTTCAAGTGCAATGGGGAA	240
Qy	286	TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCC	345
Db	241	TGGGTCCGCCAGGTCGATCACGTAATTGAACGCAGCACCGACAGCAGCAGCGGATTGCCA	300
Qy	346	ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTGAGAAAGTGTTCGGGCTGGAG	405
Db	301	ACCATGGAGGTCCGTATCAACGTATCGAGGCAGCAGGTAGAGAAAGTGTTCGGGCTGGAG	360
Qy	406	GAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC	465
Db	361	GAATACTGGTGCCAGTGTGTGGCATGGAGCTCCTCGGGTACCACCAAAAGTCAGAAGGCC	420
Qy	466	TACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG	525
Db	421	TACATCCGATTGCCATATTGCGCAAGAACTTTGAGCAGGAGCCACTGGCCAAGGAAGTG	480
Qy	526	TCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGAGGGCATCCCTCCAGCCGAG	585
Db	481	TCACTGGAGCAAGGCATTGTACTACCTTGTCGCCCCCAGAAGGAATCCCCCAGCTGAG	540
Qy	586	GTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATC	645
Db	541	GTGGAGTGGCTTCGAAATGAGGACCTCGTGGACCCCTCCCTCGATCCCAATGTGTACATC	600
Qy	646	ACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACC	705
Db	601	ACGCGGGAGCACAGCCTAGTCGTGCGTCAGGCCCGCCTGGCCGACACGGCCAACTACACC	660
Qy	706	TGCGTGGCCAAGAACATCGTGGCACGTGCGCGCAGCGCTCCGCTGCTGTCATCGTCTAC	765
Db	661	TGTGTGGCCAAGAACATCGTAGCCCGTCGCCGAAGCACCTCTGCAGCGGTCATTGTTTAT	720
Qy	766	GTGAACGGTGGGTGGTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGC	825
Db	721	GTGAACGGTGGGTGGTCGACGTGGACTGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGT	780
Qy	826	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTC	885
Db	781	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCACCTCTCAACGGGGGCGCCTTC	840
Qy	886	TGTGAGGGGCGAGAATGTCCAGAAAACAGCCTGCGCCACCC'TGTGCCAGTAGACGGCAGC	945
Db	841	TGTGAGGGGCGAGAATGTCCAGAAAACAGCCTGCGCCACTCTGTGCCAGTGGATGGGAGC	900

Qy	946	TGGAGCCCGTGGAGCAAGTGGTCGGCCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGT	1005
Db	901		
Qy	1006	TGGAGTTCGTGGAGTAAGTGGTCAGCCTGTGGGCTTGACTGCACCCACTGGCGGAGCCGC	960
Qy	1006	GAGTGCTCTGACCCAGCACCCTCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGAC	1065
Db	961		
Qy	961	GAGTGCTCTGACCCAGCACCCTCGCAATGGAGGTGAGGAGTGTCGGGGTGCTGACCTGGAC	1020
Qy	1066	ACCCGCAACTGTACCACTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCC	1125
Db	1021		
Qy	1021	ACCCGCAACTGTACCACTGACCTCTGCCTGCACACCGCTTCTTGCCCCGAGGACGTGGCT	1080
Qy	1126	CTCTATGTGGGCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCATC	1185
Db	1081		
Qy	1126	CTCTATGTGGGCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCATC	1185
Db	1081	CTCTACATCGGCCCTTGTCTGCTGTGGCTGTGTGCCTCTTCTTGCTGTTGCTGGCCCTTGA	1140
Qy	1186	CTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTC	1245
Db	1141		
Qy	1186	CTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTC	1245
Db	1141	CTCATTTACTGTGCAAGAAGGAAGGGCTGGACTCCGATGTGGCCGACTCGTCCATCCTC	1200
Qy	1246	ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCAGCAAAGCAGACAACCCCATCTGCTC	1305
Db	1201		
Qy	1246	ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCAGCAAAGCAGACAACCCCATCTGCTC	1305
Db	1201	ACCTCGGGCTTCCAGCCTGTGAGCATCAAGCCAGCAAAGCAGACAACCCCATCTGCTC	1260
Qy	1306	ACCATCCAGCCGACCTCAGCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG	1365
Db	1261		
Qy	1306	ACCATCCAGCCGACCTCAGCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG	1365
Db	1261	ACCATCCAGCCGACCTCAGCACCACCACCACCTACCAGGGCAGTCTATGTTGAGG	1320
Qy	1366	CAGGATGGGCCCAGCCCCAAGTTCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGT	1425
Db	1321		
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Db	1321	CAGGATGGACCCAGCCCCAAGTTCAGCTCTCTAATGGTCACCTGCTCAGCCCACTGGGG	1380
Qy	1426	GGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCC	1485
Db	1381		
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Db	1381	AGTGGCCGCCATACGTTGCACCACAGCTACCCACCTCTGAGGCTGAGGACTTCGTCTCC	1440
Qy	1486	CGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTAT	1545
Db	1441		
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Db	1441	CGCCTCTCCACCCAAAATACTTTTCGTTCCCTGCCCCGCGGCACCAGCAACATGGCCTAC	1500
Qy	1546	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTC	1605
Db	1501		
Qy	1546	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTC	1605
Db	1501	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACGGGGATCAGCCTCCTC	1560
Qy	1606	ATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG	1665
Db	1561		
Qy	1606	ATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG	1665
Db	1561	ATACCCCGGATGCCATACCCGAGGAAAGATCTACGAGATCTACCTCACACTGCACAAG	1620
Qy	1666	CCGGAAGACGTGAGGTTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGC	1725
Db	1621		
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Db	1621	CCAGAAGACGTGAGGTTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCAGTCGTTAGC	1680
Qy	1726	TGTGGACCCCTGGCGTCTGCTCACCCGGCCAGTCATCTGGCTATGGACCACTGTGGG	1785
Db	1681		
Qy	1726	TGTGGACCCCTGGCGTCTGCTCACCCGGCCAGTCATCTGGCTATGGACCACTGTGGG	1785
Db	1681	TGTGGGCCCCAGGAGTCCTGCTCACCCGGCCAGTCATCTTGCAATGGACCACTGTGGA	1740
Qy	1786	GAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG	1845

Db	1741	 GAGCCCAGCCCTGACAGCTGGAGTCTGCGCCTCAAAAAGCAGTCCTGCGAGGGCAGTTGG	1800
Qy	1846	GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAG	1905
Db	1801	 GAGGATGTGCTGCACCTTGGTGAGGAGTCACCTTCCCACCTCTACTACTGCCAGCTGGAG	1860
Qy	1906	GCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCC	1965
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ORIGIN

Query Match 81.8%; Score 2252.2; DB 10; Length 2697;  
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Qy	346	ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTGAGAAAGGTGTTGCGGCTGGAG	405
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Qy	406	GAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC	465
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Qy	2326	GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTC	2385
Db	2281	GCCTGCAAGGTGTGGGTGTGGCAGGTGGAGGGAGATGGGCAGAGCTTCAACATCAACTTC	2340
Qy	2386	AACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTC	2445
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AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (08-SEP-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
COMMENT Contact: MGC help desk  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Dr. Jim Lin, University of Iowa  
cDNA Library Preparation: M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada  
[info@bcgsc.bc.ca](mailto:info@bcgsc.bc.ca)  
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 126 Row: b Column: 11  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23346570.

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# ORIGIN

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Qy	1681	TTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCTGGC	1740
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Qy	1741	GTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGAC	1800
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Qy	1981	GCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAAC	2040
Db	2019	ACCAAGCGCCTCAGGCTCCTTCTGTTTGCCCTGTGGCCTGTACGTCCCTCGAGTACAAC	2078
Qy	2041	ATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAG	2100
Db	2079	ATCCGAGTGTACTGCCTGCACGACACCCACGATGCTCTCAAGGAGGTGGTGCAGCTGGAG	2138

Qy 2101 AAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTCAAGGACAGTTAC 2160  
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Qy 2161 CACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTT 2220  
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Qy 2281 TGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGG 2340  
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Qy 2641 CGGCACCTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAG 2700  
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RESULT 10

BC009333

LOCUS BC009333 2688 bp mRNA linear PRI 19-DEC-2003

DEFINITION Homo sapiens cDNA clone IMAGE:4126760, partial cds.

ACCESSION BC009333

VERSION BC009333.2 GI:40226527

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2688)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

REFERENCE 2 (bases 1 to 2688)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (12-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT On Dec 19, 2003 this sequence version replaced gi:14424611.  
Contact: MGC help desk  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc\\_mgc@nhgri.nih.gov](mailto:nisc_mgc@nhgri.nih.gov)  
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 26 Row: g Column: 22.

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# ORIGIN

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Matches 1636;   Conservative    0;   Mismatches    1;   Indels    0;   Gaps    0;

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Qy      1176 TGTCCTCATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTC 1235
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Qy      1416 CCCCTGGGTGGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGA 1475
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Db       301 CCCCTGGGTGGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGA 360

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Qy	1716	CATCGTTAGCTGTGGACCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGA	1775
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Qy	1776	CCACTGTGGGGAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGA	1835
Db	661	CCACTGTGGGGAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGA	720
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Db	721	GGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTG	780
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Qy	1956	GGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGT	2015
Db	841	GGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGT	900
Qy	2016	GGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGC	2075
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Qy	2076	ACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGACAGCTGATCCAGGAGCCACG	2135
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# RESULT 11

BD057525

LOCUS BD057525 1787 bp DNA linear PAT 27-AUG-2002

DEFINITION Netrin receptors.

ACCESSION BD057525

VERSION BD057525.1 GI:22603131

KEYWORDS JP 2001505062-A/2.

SOURCE synthetic construct

ORGANISM synthetic construct  
 artificial sequences.

REFERENCE 1 (bases 1 to 1787)

AUTHORS Lavigne,M.T., Leonardo,D.E., Hinck,L., Masu,M. and Masu,K.K.

TITLE Netrin receptors

JOURNAL Patent: JP 2001505062-A 2 17-APR-2001;  
 THE REGENTS OF THE UNIV OF CALIFORNIA

COMMENT PN JP 2001505062-A/2

PD 17-APR-2001

PF 19-FEB-1998 JP 1998536840

PR 19-FEB-1997 US 08/808982

PI MARC TESSIER LAVIGNE,DAVID E LEONARDO,LINDSAY HINCK,MASAYUKI

PI MASU,

PI KAZUKO KEINO MASU

PC C07K1/00,C07K14/00,C07K17/00,C07H21/02,C07H21/04,G01N33/53 CC

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ORIGIN

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 Best Local Similarity 98.5%; Pred. No. 2.3e-252;  
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Db	1435	AGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCAC	1494
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Db	247	GAGGTTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCC	306
Qy	1737	TGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCC	1796
Db	307	TGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCC	366
Qy	1797	TGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCT	1856
Db	367	TGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCT	426
Qy	1857	GCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTG	1916
Db	427	GCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTG	486
Qy	1917	CTACGTCTTCACCGAGCAGCTGGGCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGC	1976
Db	487	CTACGTCTTCACCGAGCAGCTGGGCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGC	546
Qy	1977	TGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTA	2036
Db	547	TGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTA	606
Qy	2037	CAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACCTCAAGGAGGTGGTGCAGCT	2096
Db	607	CAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACCTCAAGGAGGTGGTGCAGCT	666
Qy	2097	GGAGAAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTTGCACTTCAAGGACAG	2156
Db	667	GGAGAAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTTGCACTTCAAGGACAG	726
Qy	2157	TTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGGAAGAGTAAGCT	2216
Db	727	TTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGGAAGAGTAAGCT	786
Qy	2217	CCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTT	2276
Db	787	CCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTT	846
Qy	2277	GCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCT	2336
Db	847	GCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCT	906
Qy	2337	GTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAA	2396
Db	907	GTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAA	966
Qy	2397	GGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGT	2456
Db	967	GGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCAAGCCCTGGT	1026
Qy	2457	GGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGA	2516
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Qy      2517 CCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAG 2576
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# RESULT 13

MMU72634

LOCUS MMU72634 9299 bp mRNA linear ROD 13-MAY-1997

DEFINITION Mus musculus rostral cerebellar malformation protein (rcm) mRNA, complete cds.

ACCESSION U72634

VERSION U72634.1 GI:2088526

KEYWORDS .

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 9299)

AUTHORS Ackerman,S.L., Kozak,L.P., Przyborski,S.A., Rund,L.A., Boyer,B.B. and Knowles,B.B.

TITLE The mouse rostral cerebellar malformation gene encodes an UNC-5-like protein

JOURNAL Nature 386 (6627), 838-842 (1997)

MEDLINE 97271898

PUBMED 9126743

REFERENCE 2 (bases 1 to 9299)

AUTHORS Ackerman,S.L., Kozak,L.P., Rund,L.A. and Knowles,B.B.

TITLE Direct Submission

JOURNAL Submitted (25-SEP-1996) The Jackson Laboratory, 600 Main Street, Bar Harbor, ME 04609, USA

FEATURES Location/Qualifiers

source

1. .9299

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57B6/SJL"

/db\_xref="taxon:10090"

/chromosome="3"

/map="between Amy1 and Mpmv9"

gene

1. .9299

/gene="rcm"

CDS

151. .2946

/gene="rcm"

/function="transmembrane receptor"

/note="similar to C. elegans UNC-5"





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 Qy 689 ACACGGCCAACTACACCTGCGTGGCCAAGAACATCGTGGCACGTCGCCGACGCGCCTCCG 748  
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 Qy 929 GCCCAGTAGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTCCGCCCTGTGGGCTGGACTGCA 988  
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Qy 1535 ACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTA 1594  
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Qy 1715 CCATCGTTAGCTGTGGACCCCTGGCGTCTGCTCACCCGGCCAGTCATCCTGGCTATGG 1774  
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 Db 1919 CTGTGGTGAGCTGTGGGCCCTCCTGGAGTCTGCTGACCCGCCCTGTCATCCTCACTCTGC 1978

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Qy 1835 AGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACT 1894  
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Qy 1895 GCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGG 1954  
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Qy 2015 TGGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATG 2074  
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Qy 2075 CACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCAC 2134  
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Qy 2135 GGGTCCTGCACTTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCA 2194  
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Qy 2195 GCTCCCTGTGGAAGAGTAAGCTCCTTGTGCTAGCTACCAGGAGATCCCCTTTTATCACATCT 2254  
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Db 458 CCAAGAGCCGCAAGGCCTACGTCCGCATTGCATATCTCAGAAAGACTTTTGAGCAGGAGC 517  
 Qy 509 CGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGG 568  
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 Qy 1049 AGGGCACTGACCTGGACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTG 1108  
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 Db 1118 ACTCGGATGATGTTGCTCTCTACGTGGGGATTGTGATTGCTGTGATTGTGTGCCTGGCTA 1177  
 Qy 1166 TGCTGCTGCTTGTCTCATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATG 1225  
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 Db 1178 TTTCTGTGGTTGTGGCCCTGTTTGTCTATCGCAAGAACCACCGTGACTTTGAGTCAGATA 1237  
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 Db 1238 TTATCGACTCATCGGCGCTAAATGGGGGATTTCAGCCTGTTAACATCAAGGCTGCAAGAC 1297  
 Qy 1286 CAGACAACCCCCATCTGCTCACCATCCAGCCGGACCTCAGCACCACCACCACCCTACC 1345  
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 Db 1298 AAGAC-----CTCTTGGCAGTGCCACCAGACCTCACTTCTGCTGCAGCCATGTACA 1348

Qy 1346 AGGGCAGTCTCTGTCCCCGGCAGGATG-----GGCCCAGCCCCAAGTTCCAGCTCACCAA 1400  
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 Db 1469 CCCAGGATGAACTCTCTGACTTCTCCTCCAAGCTGTCCCCACAGATTACCCAGTCTCTGT 1528

Qy 1499 -----AGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCA 1534  
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 Db 1529 TGGAGAATGAGACTCTGAACGTGAAGAACCAAAGCCTTGACGGCAAACAGACCCATCCT 1588

Qy 1535 ACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTA 1594  
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Qy 1835 AGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACT 1894  
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 Db 1889 AGGGACCATGGGAGGATGTAGTGGTGGTCGGGGAGGAAAACCTTCAACCACTCCATGCTACA 1948

Qy 1895 GCCAGCTGGAGGCCAGTGCCTGCTACGTCTTACCGAGCAGCTGGGCGCCTTTGCCCTGG 1954  
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 Db 1949 TCCAGCTGGACCCAGAGGCTGTTCATATCCTGACGGAGACCCTCAGCACGTACGCCTTGG 2008

Qy 1955 TGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGG 2014  
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 Db 2009 TGGGACAATCCATCACCAAAGCAGCAGCCAAACGTCTCAAATTGGCCATCTTTGGACCAC 2068

Qy 2015 TGGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATG 2074  
 || | | | | | | | | | | | | | | | | | | | | |  
 Db 2069 TGTCTGTTCCTCACTGGAGTACAGCATCCGCGTCTACTGCCTCGATGACACACAGGATG 2128

Qy 2075 CACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCAC 2134  
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Qy 2135 GGGTCCTGCACTTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCA 2194  
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 Qy 2555 CCCAGAACTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAG 2614  
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 Db 2609 CCCACAAGCTGAAATTGGACAGGTACCTAAATTATTTTGTACGAAGTCGAGTCCCACTG 2668  
 Qy 2615 CCATGATCCTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGG 2674  
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 Db 2669 GGGTGATCCTGGATCTCTGGGAAGCCAGAATTTCCCTGATGGCAACCTGAGCATGCTGG 2728  
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 Db 2729 CAGCAGTGTGGAAGAAATGGGACGACATGAAACCGTTGTTTCTTTGGCAGCAGAAGGAA 2788  
 Qy 2735 AGTGCTGAGGCCGGC 2749  
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 Db 2789 ATTACTGATGCAGCC 2803

# RESULT 15

AB118026

LOCUS AB118026 9328 bp mRNA linear ROD 19-DEC-2003

DEFINITION Rattus norvegicus Unc5h3 mRNA, complete cds.

ACCESSION AB118026

VERSION AB118026.1 GI:40217509

KEYWORDS .

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE 1  
AUTHORS Kuramoto,T., Kuwamura,M. and Serikawa,T.  
TITLE Rat neurological mutations cerebellar vermis defect and hobble are caused by mutations in the netrin-1 receptor gene Unc5h3  
JOURNAL Mol. Brain Res. (2003) In press  
REFERENCE 2 (bases 1 to 9328)  
AUTHORS Kuramoto,T. and Serikawa,T.  
TITLE Direct Submission  
JOURNAL Submitted (22-AUG-2003) Takashi Kuramoto, Institute of Laboratory Animals, Graduate School of Medicine, Kyoto University; Yoshidakonoe-cho, Sakyo-ku, Kyoto 606-8501, Japan (E-mail:tkuramot@anim.med.kyoto-u.ac.jp, URL:www.anim.med.kyoto-u.ac.jp, Tel:81-75-753-4494, Fax:81-75-753-4409)

FEATURES Location/Qualifiers  
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# ORIGIN

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Matches 1651; Conservative 0; Mismatches 920; Indels 63; Gaps 5;



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Qy	1123	GCCCTCTATGTGGG---CCTCATCGCCGTGGCCGTCTGCCTGGTCTGCTGCTGTGTC	1179
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Db	1813	CCCCTGCGGGCCATTCTCAGGGGAGAGTCTATGAAATGTATGTGACTGTACACAGGAAA	1872
Qy	1669	GAAGACGTGAGGTTGCCCTAGCTGGCTGTGAGACCTGCTGAGTCCCATCGTTAGCTGT	1728
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Qy	1729	GGACCCCTGGCGTCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAG	1788
Db	1933	GGGCTCCTGGAGCTCTGTTGACCCGTCTGTCTCATCCTCACTCTGCATCACTGTGCAGAC	1992
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Qy 1849 GATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCC 1908  
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Qy 2269 CGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCC 2328  
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Db 2593 GTGTCAGAGGAACCTACTGGTATCGATTTGCCTCTCCTGGACCCTGCTAGCACCATTACC 2652

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Job time : 10440 secs

OM nucleic - nucleic search, using sw model

Run on: July 7, 2004, 07:48:11 ; Search time 1011 Seconds  
(without alignments)  
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Scoring table: IDENTITY\_NUC  
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Searched: 3373863 seqs, 2124099041 residues

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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5: geneseqn2001bs:\*  
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8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	2676.4	97.3	2881	6	ABK49422	Abk49422 DNA encod
4	2368.6	86.1	2907	4	AAK52261	Aak52261 Human pol
5	2356	85.6	3580	6	ABK15169	Abk15169 Human REP
6	2259	82.1	3014	2	AAV52940	Aav52940 Rat UNC-5
7	2252.2	81.8	2697	6	AAS16843	Aas16843 Rat netri

8	1562.4	56.8	1787	2	AAV52941	Aav52941	Human UNC
9	1304.2	47.4	9700	4	AAC90958	Aac90958	Plasmid p
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#### ALIGNMENTS

##### RESULT 1

ABK37922

ID ABK37922 standard; cDNA; 2752 BP.

XX

AC ABK37922;

XX

DT 21-MAY-2002 (first entry)

XX

DE cDNA encoding Human protein NOV1.

XX

KW Human; NOVX; ss; gene; cardiomyopathy; atherosclerosis; diabetes;

KW cell signal processing disorder; metabolic disorder; obesity; infection;

KW anorexia; cancer-associated cachexia; cancer; neurodegenerative disorder;

KW Alzheimer's disease; Parkinson's disease; immune disorder;

KW haematopoietic disorders; dyslipidaemia; pain; asthma; hypertension;  
 KW osteoporosis; Crohn's disease; multiple sclerosis; angina pectoris;  
 KW myocardial infarction; ulcer; allergy; benign prostatic hypertrophy;  
 KW psychosis; neurological disorder; anxiety; schizophrenia;  
 KW manic depression; dementia; dyskinesia; Huntington's disease;  
 KW Gilles de la Tourette's syndrome; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200210216-A2.  
 XX  
 PD 07-FEB-2002.  
 XX  
 PF 30-JUL-2001; 2001WO-US024225.  
 XX  
 PR 28-JUL-2000; 2000US-0221409P.  
 PR 04-AUG-2000; 2000US-0222840P.  
 PR 04-AUG-2000; 2000US-0223752P.  
 PR 04-AUG-2000; 2000US-0223762P.  
 PR 04-AUG-2000; 2000US-0223769P.  
 PR 04-AUG-2000; 2000US-0223770P.  
 PR 14-AUG-2000; 2000US-0225146P.  
 PR 15-AUG-2000; 2000US-0225392P.  
 PR 15-AUG-2000; 2000US-0225470P.  
 PR 16-AUG-2000; 2000US-0225697P.  
 PR 01-FEB-2001; 2001US-0263662P.  
 PR 05-APR-2001; 2001US-0281645P.  
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 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Padigar M, Mezes P, Mishra V, Burgess C, Casman S, Grosse WM;  
 PI Alsobrook JP, Lepley DM, Gerlach VL, Macdougall JR, Smithson G;  
 XX  
 DR WPI; 2002-180074/23.  
 DR P-PSDB; AAU85403.  
 XX  
 PT New isolated cytoplasmic, nuclear, membrane bound, or secreted  
 PT polypeptide, useful for treating cardiomyopathy, atherosclerosis,  
 PT infections, cancer, neurodegenerative, metabolic, hematopoietic and  
 PT immune disorders.  
 XX  
 PS Claim 9; Page 9-10; 213pp; English.  
 XX  
 CC The invention relates to an isolated cytoplasmic, nuclear, membrane  
 CC bound, or secreted polypeptide (NOVX, x= 1-14) their variants or mature  
 CC form. Also included are the nucleic acids encoding the NOVX proteins, a  
 CC vector comprising the nucleic acid, a cell comprising the vector, an anti  
 CC -NOVX antibody and modulators of NOVX. NOVX, the nucleic acid and the  
 CC antibody are useful for treating or preventing a NOVX-associated  
 CC disorder, where the disorder is selected from cardiomyopathy,  
 CC atherosclerosis, diabetes, a disorder related to cell signal processing  
 CC and metabolic pathway modulation, metabolic disorders, obesity,  
 CC infectious disease, anorexia, cancer-associated cachexia, cancer,  
 CC neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,  
 CC immune disorders, haematopoietic disorders, and the various  
 CC dyslipidaemias, metabolic disturbances associated with obesity, the  
 CC metabolic syndrome X and wasting disorders associated with chronic

CC diseases, bacterial, fungal, protozoal and viral infections, pain,  
CC bulimia, asthma, hypertension, urinary retention, osteoporosis, Crohn's  
CC disease, multiple sclerosis, Albright Hereditary Osteodystrophy, angina  
CC pectoris, myocardial infarction, ulcer, allergy, benign prostatic  
CC hypertrophy, and psychotic and neurological disorders, including anxiety,  
CC schizophrenia, manic depression, delirium, dementia, and dyskinesias,  
CC such as Huntington's disease and Gilles de la Tourette's syndrome. The  
CC nucleic acid is useful in gene therapy. The present sequence encodes a  
CC NOVX protein

XX

SQ Sequence 2752 BP; 505 A; 937 C; 829 G; 481 T; 0 U; 0 Other;

Query Match 100.0%; Score 2752; DB 6; Length 2752;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CCGCGGGGCCCCGCGCCCGGCCGCGCCGCTGCCGCGCCGCGGCCATGGCCGTCCGGCCCC 60
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Qy     61 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 120
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Db     61 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 120

Qy    121 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCCTGGTGCCAACCCGGACCTGCTTCCCCAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCCTGGTGCCAACCCGGACCTGCTTCCCCAC 180

Qy    181 TTCCTGGTGGAGCCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TTCCTGGTGGAGCCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240

Qy    241 AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 300

Qy    301 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGC 360

Qy    361 ATTAATGTCTCAAGGCAGCAGGTTCGAGAAGGTGTTTCGGGCTGGAGGAATACTGGTGCCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATTAATGTCTCAAGGCAGCAGGTTCGAGAAGGTGTTTCGGGCTGGAGGAATACTGGTGCCAG 420

Qy    421 TGCCTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TGCCTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 480

Qy    481 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 540

Qy    541 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600

Qy    601 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 660
```



Db	601	 AACGAGGACCTGGTGGACCCGTCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC	660
Qy	661	CTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC	720
Db	661	 CTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC	720
Qy	721	ATCGTGGCACGTCGCCGAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG	780
Db	721	 ATCGTGGCACGTCGCCGAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG	780
Qy	781	TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG	840
Db	781	 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG	840
Qy	841	AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT	900
Db	841	 AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT	900
Qy	901	GTCCAGAAAACAGCCTGCGCCACCCTGTGCCAGTAGACGGCAGCTGGAGCCCGTGGAGC	960
Db	901	 GTCCAGAAAACAGCCTGCGCCACCCTGTGCCAGTAGACGGCAGCTGGAGCCCGTGGAGC	960
Qy	961	AAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCA	1020
Db	961	 AAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCA	1020
Qy	1021	GCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACC	1080
Db	1021	 GCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACC	1080
Qy	1081	AGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTC	1140
Db	1081	 AGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTC	1140
Qy	1141	ATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCCTCATCCTCGTTTATTGCCGG	1200
Db	1141	 ATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCCTCATCCTCGTTTATTGCCGG	1200
Qy	1201	AAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTCCAG	1260
Db	1201	 AAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTCCAG	1260
Qy	1261	CCCGTCAGCATCAAGCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCGGAC	1320
Db	1261	 CCCGTCAGCATCAAGCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCGGAC	1320
Qy	1321	CTCAGCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCCAGC	1380
Db	1321	 CTCAGCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCCAGC	1380
Qy	1381	CCCAAGTTCCAGCTACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACACA	1440
Db	1381	 CCCAAGTTCCAGCTACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACACA	1440
Qy	1441	CTGCACCACAGCTCTCCACCTCTGAGGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAG	1500

Db 1441 CTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCTCTCCCGCCTCTCCACCCAG 1500

Qy 1501 AACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTC 1560  
 |||

Db 1501 AACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTC 1560

Qy 1561 CTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCC 1620  
 |||

Db 1561 CTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCC 1620

Qy 1621 ATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGG 1680  
 |||

Db 1621 ATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGG 1680

Qy 1681 TTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCTGGC 1740  
 |||

Db 1681 TTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCTGGC 1740

Qy 1741 GTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGAC 1800  
 |||

Db 1741 GTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGAC 1800

Qy 1801 AGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCAC 1860  
 |||

Db 1801 AGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCAC 1860

Qy 1861 CTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTAC 1920  
 |||

Db 1861 CTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTAC 1920

Qy 1921 GTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCC 1980  
 |||

Db 1921 GTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCC 1980

Qy 1981 GCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAAC 2040  
 |||

Db 1981 GCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAAC 2040

Qy 2041 ATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAG 2100  
 |||

Db 2041 ATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAG 2100

Qy 2101 AAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTCAAGGACAGTTAC 2160  
 |||

Db 2101 AAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTCAAGGACAGTTAC 2160

Qy 2161 CACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTT 2220  
 |||

Db 2161 CACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTT 2220

Qy 2221 GTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCAC 2280  
 |||

Db 2221 GTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCAC 2280

Qy 2281 TGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGG 2340  
 |||

Db 2281 TGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGG 2340



```

Qy      2341 GTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAGGAC 2400
          |||
Db      2341 GTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAGGAC 2400

Qy      2401 ACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGC 2460
          |||
Db      2401 ACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGC 2460

Qy      2461 CCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGACCCA 2520
          |||
Db      2461 CCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGACCCA 2520

Qy      2521 CCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAGCCAT 2580
          |||
Db      2521 CCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAGCCAT 2580

Qy      2581 CTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCG 2640
          |||
Db      2581 CTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCG 2640

Qy      2641 CGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAG 2700
          |||
Db      2641 CGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAG 2700

Qy      2701 CCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGAGGCCGGCCAG 2752
          |||
Db      2701 CCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGAGGCCGGCCAG 2752

```

# RESULT 2

ABK52891

ID ABK52891 standard; DNA; 2697 BP.

XX

AC ABK52891;

XX

DT 27-AUG-2002 (first entry)

XX

DE Human netrin binding membrane receptor UNC5H-1 DNA sequence #1.

XX

KW Netrin binding membrane receptor; receptor; UNC5H-1; gene; ds; human;

KW nootropic; neuroprotective; cytostatic; antiparkinsonian;

KW cerebroprotective; cancer; central nervous system; CNS; stroke;

KW Parkinson's disease; multiple sclerosis; Alzheimer's disease.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..2697

FT /\*tag= a

FT /product= "Netrin binding membrane receptor UNC5H-1"

XX

PN WO200233080-A2.

XX

PD 25-APR-2002.

XX

PF 15-OCT-2001; 2001WO-EP011891.

XX  
 PR 16-OCT-2000; 2000US-0240061P.  
 XX  
 PA (FARB ) BAYER AG.  
 XX  
 PI Koehler RH;  
 XX  
 DR WPI; 2002-463314/49.  
 DR P-PSDB; AAU97899.  
 XX  
 PT Novel human netrin binding membrane receptor polypeptide and  
 PT polynucleotides for identifying modulating agents useful in treating  
 PT diseases e.g. Parkinson's disease, multiple sclerosis, stroke,  
 PT Alzheimer's disease.  
 XX  
 PS Claim 1; Fig 1; 94pp; English.  
 XX  
 CC This invention relates to the DNA and protein sequences of a novel  
 CC purified human netrin binding membrane receptor, UNC5H-1. The DNA  
 CC sequence of the invention is useful as a probe for detecting a nucleic  
 CC acid encoding the UNC5H-1 protein in a biological sample. The sequences  
 CC of the invention are useful to screen for agents which decrease the  
 CC activity of the UNC5H-1 protein. The sequences are also useful for  
 CC screening agents which regulate (modulate) the activity of the protein of  
 CC the invention. A pharmaceutical composition containing the protein of the  
 CC invention or a reagent that modulates the activity of the UNC5H-1 protein  
 CC may be useful for treating a UNC5H-1 dysfunction related disease such as  
 CC cancer or a central nervous system (CNS) disorders (e.g, Parkinson's  
 CC disease, multiple sclerosis, stroke and Alzheimer's disease). Fusion  
 CC proteins comprising the UNC5H-1 protein are useful for generating  
 CC antibodies and for in various assay systems, and the protein can be used  
 CC as a bait protein in a two-hybrid assay or three-hybrid assay. The method  
 CC of the invention is useful for detecting a coding sequence for the UNC5H-  
 CC 1 protein. The present sequence represents a DNA sequence encoding the  
 CC human netrin binding membrane receptor UNC5H-1 protein of the invention  
 XX  
 SQ Sequence 2697 BP; 503 A; 906 C; 807 G; 481 T; 0 U; 0 Other;

Query Match 97.7%; Score 2687.4; DB 6; Length 2697;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 2691; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy	46	ATGGCCGTC	CGGCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTC	105
Db	1	ATGGCCGTC	CGGCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTC	60
Qy	106	CGCGGCTCGGGTGCC	CAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCG	165
Db	61	CGCGGCTCGGGTGCC	CAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCG	120
Qy	166	GACCTGCTTCCCCACTT	CCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAGCCA	225
Db	121	GACCTGCTTCCCCACTT	CCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAGCCA	180
Qy	226	GTGCTGCTTGTGTGCA	AGGCCGTGCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAG	285
Db	181	GTGCTGCTTGTGTGCA	AGGCCGTGCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAG	240

Qy	286	TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCC	345
Db	241	TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCC	300
Qy	346	ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCTGGGCTGGAG	405
Db	301	ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCTGGGCTGGAG	360
Qy	406	GAATACTGGTGCCAGTGCCTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC	465
Db	361	GAATACTGGTGCCAGTGCCTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC	420
Qy	466	TACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG	525
Db	421	TACATCCGCATAGCCTATTTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG	480
Qy	526	TCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGAGGGCATCCCTCCAGCCGAG	585
Db	481	TCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGAGGGCATCCCTCCAGCCGAG	540
Qy	586	GTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATC	645
Db	541	GTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATC	600
Qy	646	ACGCGGGAGCACAGCCTGGTGGTGCACAGGCCCGCCTTGCTGACACGGCCAACTACACC	705
Db	601	ACGCGGGAGCACAGCCTGGTGGTGCACAGGCCCGCCTTGCTGACACGGCCAACTACACC	660
Qy	706	TGCGTGGCCAAGAACATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTTCATCGTCTAC	765
Db	661	TGCGTGGCCAAGAACATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTTCATCGTCTAC	720
Qy	766	GTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGC	825
Db	721	GTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGC	780
Qy	826	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTC	885
Db	781	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTC	840
Qy	886	TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGC	945
Db	841	TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTGGACGGCAGC	900
Qy	946	TGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGT	1005
Db	901	TGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGT	960
Qy	1006	GAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGAC	1065
Db	961	GAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGAC	1020
Qy	1066	ACCCGCAACTGTACCACTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCC	1125
Db	1021	ACCCGCAACTGTACCACTGACCTCTGTGTACACACTGCTTCTGGCCCTGAGGACGTGGCC	1080

Qy	1126	CTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCTGCTGCTTGTCCTCATC	1185
Db	1081	CTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCTGCTGCTTGTCCTCATC	1140
Qy	1186	CTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTC	1245
Db	1141	CTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTC	1200
Qy	1246	ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTC	1305
Db	1201	ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTC	1260
Qy	1306	ACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG	1365
Db	1261	ACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG	1320
Qy	1366	CAGGATGGGCCCAGCCCCAAGTTCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGT	1425
Db	1321	CAGGATGGGCCCAGCCCCAAGTTCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGT	1380
Qy	1426	GGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCC	1485
Db	1381	GGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCC	1440
Qy	1486	CGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTAT	1545
Db	1441	CGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTAT	1500
Qy	1546	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTC	1605
Db	1501	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGAATCAGCCTCCTC	1560
Qy	1606	ATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG	1665
Db	1561	ATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG	1620
Qy	1666	CCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGC	1725
Db	1621	CCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGC	1680
Qy	1726	TGTGGACCCCTGGCGTCTGCTCACC CGCCAGTCATCCTGGCTATGGACCACTGTGGG	1785
Db	1681	TGTGGACCCCTGGCGTCTGCTCACC CGCCAGTCATCCTGGCTATGGACCACTGTGGG	1740
Qy	1786	GAGCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG	1845
Db	1741	GAGCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG	1800
Qy	1846	GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAG	1905
Db	1801	GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAG	1860
Qy	1906	GCCAGTGCCCTGCTACGTCTTACCGAGCAGCTGGGCGCCTTTGCCCTGGTGGGAGAGGCC	1965
Db	1861	GCCAGTGCCCTGCTACGTCTTACCGAGCAGCTGGGCGCCTTTGCCCTGGTGGGAGAGGCC	1920
Qy	1966	CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC	2025

Db	1921	CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC	1980
Qy	2026	TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG	2085
Db	1981	TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG	2040
Qy	2086	GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCAC	2145
Db	2041	GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCAC	2100
Qy	2146	TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGG	2205
Db	2101	TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGG	2160
Qy	2206	AAGAGTAAGCTCCTTGTCTAGCTACCAGGAGATCCCCCTTTATCACATCTGGAATGGCACG	2265
Db	2161	AAGAGTAAGCTCCTTGTCTAGCTACCAGGAGATCCCCCTTTATCACATCTGGAATGGCACG	2220
Qy	2266	CAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTG	2325
Db	2221	CAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTG	2280
Qy	2326	GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTC	2385
Db	2281	GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTC	2340
Qy	2386	AACATCACCAAGGACACAAGGTTTGTCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTC	2445
Db	2341	AACATCACCAAGGACACAAGGTTTGTCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTC	2400
Qy	2446	CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCCTTCCTCATTCGGCAGAAGATAATT	2505
Db	2401	CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCCTTCCTCATTCGGCAGAAGATAATT	2460
Qy	2506	TCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTC	2565
Db	2461	TCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTC	2520
Qy	2566	CACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTC	2625
Db	2521	CACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTC	2580
Qy	2626	AACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTG	2685
Db	2581	AACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTG	2640
Qy	2686	GCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTGCGAGGCTGAGTGCTGA	2742
Db	2641	GCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTGCGAGGCTGAGTGCTGA	2697

RESULT 3

ABK49422

ID ABK49422 standard; DNA; 2881 BP.

XX

AC ABK49422;

XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE DNA encoding human UNC5-like protein NOV1.  
 XX  
 KW Human; NOVX polypeptide; cardiomyopathy; atherosclerosis; cancer;  
 KW cell signal processing; metabolic pathway modulation; cancerous tissue;  
 KW antibody; diabetes; transgenic animal; UNC5-like protein; NOV1;  
 KW chromosome 13; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 87. .2786  
 FT /\*tag= a  
 FT /product= "Human UNC5-like protein NOV1"  
 XX  
 PN WO200229038-A2.  
 XX  
 PD 11-APR-2002.  
 XX  
 PF 04-OCT-2001; 2001WO-US031377.  
 XX  
 PR 04-OCT-2000; 2000US-0237862P.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Herrmann JL, Rastelli L, Shimkets RA;  
 XX  
 DR WPI; 2002-340104/37.  
 DR P-PSDB; AAU79939.  
 XX  
 PT Novel isolated NOVX polypeptide, and encoded polynucleotide, useful for  
 PT treating cardiomyopathy, atherosclerosis, and cancer.  
 XX  
 PS Claim 8; Page 7-8; 180pp; English.  
 XX  
 CC The present invention relates to a new NOVX polypeptide having a 900  
 CC (NOV1), 4349 (NOV2), 940 (NOV3), 798 (NOV4), 865 (NOV5), or 331 (NOV6)  
 CC residue amino acid sequence, as given in the specification. The novel  
 CC polypeptide, and its encoding polynucleotide, are used to treat  
 CC cardiomyopathy, atherosclerosis, cancer or a disease related to cell  
 CC signal processing and metabolic pathway modulation, in a human. Detecting  
 CC the polypeptide or polynucleotide is useful for identifying cancerous  
 CC tissue. The antibody can be used to treat diabetes or cancer. The host  
 CC cells can be used to produce non-human transgenic animals useful in drug  
 CC screening. The present nucleic acid sequence is that of the human UNC5-  
 CC like NOV1 gene located on chromosome 13. This sequence encodes the human  
 CC UNC5-like protein NOV1 of the invention  
 XX  
 SQ Sequence 2881 BP; 526 A; 985 C; 868 G; 502 T; 0 U; 0 Other;  
  
 Query Match 97.3%; Score 2676.4; DB 6; Length 2881;  
 Best Local Similarity 98.9%; Pred. No. 0;  
 Matches 2728; Conservative 0; Mismatches 21; Indels 9; Gaps 3;  
  
 Qy 1 CCGCGGGGCCCCGCGCCCGGCCCGCCGCTGCCCGCCCGCGGCCATGGCCGTCCGGCCCC 60



Db	42	 CCGCGGGGCCCCGCGCCCGGCCCGCCCGCCTGCCCGCCCGCGGCCATGGCCGTCCGGCCCC	101
Qy	61	GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC	120
Db	102	 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC	161
Qy	121	CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCCTGGTGCCAACCCGGACCTGCTTCCCCAC	180
Db	162	 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCCTGGTGCCAACCCGGACCTGCTTCCCCAC	221
Qy	181	TTCCTGGTGGAGCCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC	240
Db	222	 TTCCTGGTGGAGCCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC	281
Qy	241	AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG	300
Db	282	 AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG	341
Qy	301	GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCACCATGGAGGTCCGC	360
Db	342	 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGTGAGCCGACCATGGAGGTCCGC	401
Qy	361	ATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTTCGGGCTGGAGGAATACTGGTGCCAG	420
Db	402	 ATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTTCGGGCTGGAGGAATACTGGTGCCAG	461
Qy	421	TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC	480
Db	462	 TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC	521
Qy	481	AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC	540
Db	522	 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC	581
Qy	541	ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG	600
Db	582	 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG	641
Qy	601	AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC	660
Db	642	 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC	701
Qy	661	CTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC	720
Db	702	 CTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC	761
Qy	721	ATCGTGGCACGTGCGCGCAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG	780
Db	762	 ATCGTGGCACGTGCGCGCAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG	821
Qy	781	TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG	840
Db	822	 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG	881
Qy	841	AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGCGCTTTCTGTGAGGGGCAGAAT	900

Db	882	AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT	941
Qy	901	GTCCAGAA--AACAGCCTGCGCCACCCTGTGCCAGTAGACGGCAGCTGGAGCCCGTGG	957
Db	942	GTCCATGACCGCACCGTCTCCTCTCTGCTTGTCTCTGTGGACGGCAGCTGGAGCCCGTGG	1001
Qy	958	AGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGAC	1017
Db	1002	AGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGAC	1061
Qy	1018	CCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGT	1077
Db	1062	CCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGT	1121
Qy	1078	ACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGC	1137
Db	1122	ACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGC	1181
Qy	1138	CTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCTATCCTCGTTTATTGC	1197
Db	1182	CTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCTATCCTCGTTTATTGC	1241
Qy	1198	CGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTC	1257
Db	1242	CGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTC	1301
Qy	1258	CAGCCCGTCAGCATCAAGCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCG	1317
Db	1302	CAGCCCGTCAGCATCAAGCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCG	1361
Qy	1318	GACCTCAGCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCC	1377
Db	1362	GACCTCAG---CACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCC	1418
Qy	1378	AGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCAC	1437
Db	1419	AGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCAC	1478
Qy	1438	AACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACC	1497
Db	1479	AACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACC	1538
Qy	1498	CAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAAC	1557
Db	1539	CAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAAC	1598
Qy	1558	TTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGAT	1617
Db	1599	TTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGAT	1658
Qy	1618	GCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTG	1677
Db	1659	GCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTG	1718
Qy	1678	AGGTTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCT	1737
Db	1719	AGGTTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCT	1778

Qy	1738	GGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCT	1797
Db	1779	GGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCT	1838
Qy	1798	GACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGG---AGGATGTG	1854
Db	1839	GACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGCAGGATGTG	1898
Qy	1855	CTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCC	1914
Db	1899	CTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCC	1958
Qy	1915	TGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTG	1974
Db	1959	TGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTG	2018
Qy	1975	GCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAG	2034
Db	2019	GCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAG	2078
Qy	2035	TACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAG	2094
Db	2079	TACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAG	2138
Qy	2095	CTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTCAAGGAC	2154
Db	2139	CTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTCAAGGAC	2198
Qy	2155	AGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAG	2214
Db	2199	AGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAG	2258
Qy	2215	CTCCTTGTGAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTAC	2274
Db	2259	CTCCTTGTGAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTAC	2318
Qy	2275	TTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAG	2334
Db	2319	TTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAG	2378
Qy	2335	CTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACC	2394
Db	2379	CTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACC	2438
Qy	2395	AAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTG	2454
Db	2439	AAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTG	2498
Qy	2455	GTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTG	2514
Db	2499	GTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTG	2558
Qy	2515	GACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGAC	2574
Db	2559	GACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGAC	2618

Qy 2575 AGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGG 2634  
 |||  
 Db 2619 AGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGG 2678  
 Qy 2635 GAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTG 2694  
 |||  
 Db 2679 GAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTG 2738  
 Qy 2695 GGCCAGCCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGAGGCCGGCCAG 2752  
 |||  
 Db 2739 GGCCAGCCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGAGGCCGGCCAG 2796

RESULT 4

AAK52261

ID AAK52261 standard; cDNA; 2907 BP.

XX

AC AAK52261;

XX

DT 06-NOV-2001 (first entry)

XX

DE Human polynucleotide SEQ ID NO 806.

XX

KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KW nervous system disorder; arthritis; inflammation; ss.

XX

OS Homo sapiens.

XX

PN WO200157190-A2.

XX

PD 09-AUG-2001.

XX

PF 05-FEB-2001; 2001WO-US004098.

XX

PR 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

PR 20-JUN-2000; 2000US-00598075.

PR 19-JUL-2000; 2000US-00620325.

PR 01-SEP-2000; 2000US-00654936.

PR 15-SEP-2000; 2000US-00663561.

PR 20-OCT-2000; 2000US-00693325.

PR 30-NOV-2000; 2000US-00728422.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;  
 PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;  
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

XX

DR WPI; 2001-476283/51.

DR P-PSDB; AAM79128.

XX

PT Nucleic acids encoding polypeptides with cytokine-like activities, useful  
 PT in diagnosis and gene therapy.

XX



Qy	632	CCAATGTATACATCACGCGGGAGCACAGCCTGGTGGTGC	691
Db	710	CCAATGTATACATCACGCGGGAGCACAGCCTGGTGGTGC	769
Qy	692	CGGCCAACTACACCTGCGTGGCCAAGAACATCGTGGCACGT	751
Db	770	CGGCCAACTACACCTGCGTGGCCAAGAACATCGTGGCACGT	829
Qy	752	CTGTCATCGTCTAC-----	765
Db	830	CTGTCATCGTCTACGGTGGGCCCCGGGACTCCCTGGT	889
Qy	766	-----GTGAACGGTGGGTGGT	784
Db	890	CCCTGGGCAGTGACATGTGGCTGTCTTCTCTGTCCGCCAGT	949
Qy	785	CGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCT	844
Db	950	CGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCT	1009
Qy	845	GGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGT	904
Db	1010	GGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGT	1069
Qy	905	AGAAAACAGCCTGCGCCACCCTGTGCCAGTAGACGGCAGCTGGAGCCC	964
Db	1070	AGAAAACAGCCTGCGCCACCCTGTGCCAGTAGACGGCAGCTGGAGCCC	1129
Qy	965	GGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCT	1024
Db	1130	GGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCT	1189
Qy	1025	CCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACT	1084
Db	1190	CCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACT	1249
Qy	1085	ACCTCTGTGTACACA-----	1099
Db	1250	ACCTCTGTGTACACAACCTCTACACCCCTGCCCCACCAAGGCCATGCTGTCT	1309
Qy	1100	GTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCC	1159
Db	1310	CTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCC	1369
Qy	1160	TGGTCCTGCTGCTGCTTGTCTCATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACT	1219
Db	1370	TGGTCCTGCTGCTGCTTGTCTCATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACT	1429
Qy	1220	CAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCA	1279
Db	1430	CAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCA	1489
Qy	1280	GCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCGGACCTCAGCACCACCACCACCA	1339
Db	1490	GCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCGGACCTCAGCACCACCACCACCA	1549

Qy	1340	CCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCA	1399
Db	1550	CCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCA	1609
Qy	1400	ATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACACACTGCACCACAGCTCTCCCA	1459
Db	1610	ATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACACACTGCACCACAGCTCTCCCA	1669
Qy	1460	CCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGC	1519
Db	1670	CCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGC	1729
Qy	1520	CCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGA	1579
Db	1730	CCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGA	1789
Qy	1580	TCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCCATACCCCGAGGGAAGATCT	1639
Db	1790	TCCCTAATACAGGAATCAGCCTCCTCATCCCCCAGATGCCATACCCCGAGGGAAGATCT	1849
Qy	1640	ATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGGTTGCCCCTAGCTGGCTGTC	1699
Db	1850	ATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTG-----	1887
Qy	1700	AGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAG	1759
Db	1888	-----AGCTGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAG	1924
Qy	1760	TCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCA	1819
Db	1925	TCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCA	1984
Qy	1820	AAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCT	1879
Db	1985	AAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCT	2044
Qy	1880	CCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGG	1939
Db	2045	CCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGG	2104
Qy	1940	GCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGC	1999
Db	2105	GCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGC	2164
Qy	2000	TTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGC	2059
Db	2165	TTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGC	2224
Qy	2060	ATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGC	2119
Db	2225	ATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGC	2284
Qy	2120	TGATCCAGGAGCCACGGGTCCTGCACTTCAAGGACAGTTACCACAACCTGCGCCTATCCA	2179
Db	2285	TGATCCAGGAGCCACGGGTCCTGCACTTCAAGGACAGTTACCACAACCTGCGCCTATCCA	2344
Qy	2180	TCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTTGTGAGCTACCAGGAGATCC	2239

Db	2345		TCCACGATGTGCCAGCTCCCTGTGGAAGAGTAAGCTCCTTGTCAAGTACCAGGAGATCC	2404
Qy	2240		CCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCACTGCACCTTCACCCTGGAGC	2299
Db	2405		CCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCACTGCACCTTCACCCTGGAGC	2464
Qy	2300		GTGTCAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCG	2359
Db	2465		GTGTCAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCG	2524
Qy	2360		ACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAGGACACAAGGTTTGCTGAGCTGC	2419
Db	2525		ACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAGGACACAAGGTTTGCTGAGCTGC	2584
Qy	2420		TGGCTCTGGAGAGTGAAGCGGGGTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCC	2479
Db	2585		TGGCTCTGGAGAGTGAAGCGGGGTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCC	2644
Qy	2480		CCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCG	2539
Db	2645		CCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCG	2704
Qy	2540		ACTGGCGGACTCTGGCCAGAACTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCA	2599
Db	2705		ACTGGCGGACTCTGGCCAGAACTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCA	2764
Qy	2600		AGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCGGGCACTTCCCCAACGGCA	2659
Db	2765		AGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCGGGCACTTCCCCAACGGCA	2824
Qy	2660		ACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCA	2719
Db	2825		ACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCA	2884
Qy	2720		CAGTGTCTGGAGGCTGAGTGCTGA	2742
Db	2885		CAGTGTCTGGAGGCTGAGTGCTGA	2907

RESULT 5

ABK15169

ID ABK15169 standard; DNA; 3580 BP.

XX

AC ABK15169;

XX

DT 23-APR-2002 (first entry)

XX

DE Human REPTR 1 cDNA sequence.

XX

KW REPTR; human; antiinflammatory; cytostatic; immunosuppressive; antiviral;  
 KW anti-HIV; antiarthritic; anticonvulsant; nootropic; neuroprotective;  
 KW antiallergic; antibody; immunogen; endometriosis;  
 KW gastrointestinal disorder; gastritis; oesophageal carcinoma;  
 KW Crohn's disease; irritable bowel syndrome; ulcerative colitis;  
 KW endocrine disorder; hypothalamus disorder; Kallman's disease;  
 KW autoimmune disease; inflammatory disease; infertility; receptor;



KW acquired immune deficiency syndrome; AIDS; rheumatoid arthritis; allergy;  
 KW osteoarthritis; diabetes mellitus; multiple sclerosis;  
 KW systemic lupus erythematosus; cell proliferative disorder; cancer;  
 KW developmental disorder; Duchenne muscular dystrophy; gene;  
 KW Becker muscular dystrophy; neurological disorder; epilepsy;  
 KW Alzheimer's disease; Huntington's disease; reproductive disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 4. .2532  
 FT /\*tag= a  
 FT /product= "REPTR1 protein"  
 XX  
 PN WO200198354-A2.  
 XX  
 PD 27-DEC-2001.  
 XX  
 PF 21-JUN-2001; 2001WO-US019942.  
 XX  
 PR 21-JUN-2000; 2000US-0214027P.  
 PR 25-AUG-2000; 2000US-0228045P.  
 PR 12-DEC-2000; 2000US-0255104P.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 XX  
 PI Griffin JA, Kallick DA, Tribouley CM, Yue H, Nguyen DB, Tang YT;  
 PI Lal P, Policky JL, Azimzai Y, Lu DAM, Graul R, Yao MG, Burford N;  
 PI Hafalia AJA, Baughn MR, Bandman O, Patterson C, Yang J, Xu Y;  
 PI Gandhi AR, Warren BA, Ding L, Sanjanwala MS, Duggan BM, Lu Y;  
 XX  
 DR WPI; 2002-090432/12.  
 DR P-PSDB; AAU17818.  
 XX  
 PT Twelve human receptors (referred to as REPTR-1 to REPTR-12), useful in  
 PT the diagnosis, treatment and prevention of gastrointestinal (e.g.  
 PT gastritis), autoimmune/inflammatory (e.g. osteoarthritis) and cell  
 PT proliferative (e.g. cancer) disorders.  
 XX  
 PS Claim 57; Page 142-143; 157pp; English.  
 XX  
 CC This invention relates to twelve human receptors cDNA sequences referred  
 CC to as REPTR-1 to REPTR-12), and the proteins encoded thereby. The  
 CC proteins of the invention may have antiinflammatory, cytostatic,  
 CC immunosuppressive, antiviral, anti-HIV, antiarthritic, muscular active  
 CC general, anticonvulsant, nootropic, neuroprotective, antiallergic  
 CC activities. The sequences of the invention may be used to produce REPTR  
 CC agonists or antagonists, and the protein sequences may be used to raise  
 CC anti-REPTR antibodies. These molecules and the REPTR polynucleotides and  
 CC polypeptides of the invention are useful in the diagnosis, treatment and  
 CC prevention of gastrointestinal (e.g. gastritis, oesophageal carcinoma,  
 CC Crohn's disease, irritable bowel syndrome, ulcerative colitis), endocrine  
 CC (e.g. hypothalamus disorder, Kallman's disease), autoimmune/ inflammatory  
 CC (e.g. acquired immune deficiency syndrome (AIDS), rheumatoid arthritis,  
 CC allergies, osteoarthritis, diabetes mellitus, multiple sclerosis,  
 CC systemic lupus erythematosus), cell proliferative (e.g. cancer),  
 CC developmental (e.g. Duchenne and Becker muscular dystrophy), neurological

CC (e.g. epilepsy, Alzheimer's disease, Huntington's disease) and  
CC reproductive (e.g. infertility, endometriosis) disorders. Numerous other  
CC examples of each disorder are given in the specification. The present  
CC sequence represents the human REPTR1 cDNA sequence of the invention  
XX

SQ Sequence 3580 BP; 670 A; 1233 C; 1025 G; 652 T; 0 U; 0 Other;

Query Match 85.6%; Score 2356; DB 6; Length 3580;  
Best Local Similarity 93.6%; Pred. No. 0;  
Matches 2537; Conservative 0; Mismatches 5; Indels 168; Gaps 1;

```
Qy      43 GCCATGGCCGTCCGGCCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGG 102
      |||
Db       1 GCCATGGCCGTCCGGCCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGG 60

Qy     103 CTCCGCGGCTCGGGTGCCCGAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAAC 162
      |||
Db      61 CTCCGCGGCTCGGGTGCCCGAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAAC 120

Qy     163 CCGGACCTGCTTCCCCACTTCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAG 222
      |||
Db     121 CCGGACCTGCTTCCCCACTTCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAG 180

Qy     223 CCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGG 282
      |||
Db     181 CCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGG 240

Qy     283 GAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTG 342
      |||
Db     241 GAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTG 300

Qy     343 CCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCCGGGCTG 402
      |||
Db     301 CCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCCGGGCTG 360

Qy     403 GAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAG 462
      |||
Db     361 GAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAG 420

Qy     463 GCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAG 522
      |||
Db     421 GCCTACATCCGCATAGCCATTTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAG 480

Qy     523 GTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGAGGGCATCCCTCCAGCC 582
      |||
Db     481 GTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGAGGGCATCCCTCCAGCC 540

Qy     583 GAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATAC 642
      |||
Db     541 GAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATAC 600

Qy     643 ATCACGCGGGAGCACAGCCTGGTGGTGCACAGGCCCGCCTTGCTGACACGGCCAACACTAC 702
      |||
Db     601 ATCACGCGGGAGCACAGCCTGGTGGTGCACAGGCCCGCCTTGCTGACACGGCCAACACTAC 660

Qy     703 ACCTGCGTGGCCAAGAACATCGTGGCACGTCGCCGCGAGCGCCTCCGCTGCTGTCATCGTC 762
      |||
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Db	661	ACCTGCGTGGCCAAGAACATCGTGGCACGTGCGCCGAGCGCCTCCGCTGCTGTCATCGTC	720
Qy	763	TACGTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGG	822
Db	721	TACGTG-----	726
Qy	823	CGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCT	882
Db	727	-----	726
Qy	883	TTCTGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCAGTAGACGGC	942
Db	727	-----GACGGC	732
Qy	943	AGCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGC	1002
Db	733	AGCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGC	792
Qy	1003	CGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTG	1062
Db	793	CGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTG	852
Qy	1063	GACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTG	1122
Db	853	GACACCCGCAACTGTACCAGTGACCTCTGTGTACACACTGCTTCTGGCCCTGAGGACGTG	912
Qy	1123	GCCCTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTC	1182
Db	913	GCCCTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTC	972
Qy	1183	ATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATT	1242
Db	973	ATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATT	1032
Qy	1243	CTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTG	1302
Db	1033	CTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTG	1092
Qy	1303	CTCACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCC	1362
Db	1093	CTCACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCC	1152
Qy	1363	CGGCAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTG	1422
Db	1153	CGGCAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTG	1212
Qy	1423	GGTGGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTC	1482
Db	1213	GGTGGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTC	1272
Qy	1483	TCCCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACC	1542
Db	1273	TCCCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACC	1332
Qy	1543	TATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTC	1602
Db	1333	TATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGAATCAGCCTC	1392

Qy	1603	CTCATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCAC	1662
Db	1393	CTCATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCAC	1452
Qy	1663	AAGCCGGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTT	1722
Db	1453	AAGCCGGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTT	1512
Qy	1723	AGCTGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGT	1782
Db	1513	AGCTGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGT	1572
Qy	1783	GGGGAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGC	1842
Db	1573	GGGGAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGC	1632
Qy	1843	TGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTG	1902
Db	1633	TGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTG	1692
Qy	1903	GAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAG	1962
Db	1693	GAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAG	1752
Qy	1963	GCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGC	2022
Db	1753	GCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGC	1812
Qy	2023	ACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAG	2082
Db	1813	ACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAG	1872
Qy	2083	GAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTTG	2142
Db	1873	GAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTTG	1932
Qy	2143	CACTTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTG	2202
Db	1933	CACTTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTG	1992
Qy	2203	TGGAAGAGTAAGCTCCTTGTGACGTACCAGGAGATCCCCTTTTATCACATCTGGAATGGC	2262
Db	1993	TGGAAGAGTAAGCTCCTTGTGACGTACCAGGAGATCCCCTTTTATCACATCTGGAATGGC	2052
Qy	2263	ACGCAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGAC	2322
Db	2053	ACGCAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGAC	2112
Qy	2323	CTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAAC	2382
Db	2113	CTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAAC	2172
Qy	2383	TTCAACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGG	2442
Db	2173	TTCAACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGG	2232

Qy 2443 GTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTGCGCAGAAGATA 2502  
 |||  
 Db 2233 GTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTGCGCAGAAGATA 2292  
 Qy 2503 ATTTCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAA 2562  
 |||  
 Db 2293 ATTTCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAA 2352  
 Qy 2563 CTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATC 2622  
 |||  
 Db 2353 CTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATC 2412  
 Qy 2623 CTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCA 2682  
 |||  
 Db 2413 CTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCA 2472  
 Qy 2683 GTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGA 2742  
 |||  
 Db 2473 GTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGA 2532  
 Qy 2743 GGCCGGCCAG 2752  
 |||  
 Db 2533 GGCCGGCCAG 2542

RESULT 6

AAV52940

ID AAV52940 standard; cDNA; 3014 BP.

XX

AC AAV52940;

XX

DT 25-MAR-2003 (revised)

DT 21-DEC-1998 (first entry)

XX

DE Rat UNC-5 homologue unc5h-1 cDNA.

XX

KW UNC-5; UNC5H-1; rat; netrin receptor; cell migration; axon guidance;  
 KW diagnosis; therapy; ds.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT CDS 1..2697

FT /\*tag= a

XX

PN WO9837085-A1.

XX

PD 27-AUG-1998.

XX

PF 19-FEB-1998; 98WO-US003143.

XX

PR 19-FEB-1997; 97US-00808982.

XX

PA (REGC ) UNIV CALIFORNIA.

XX

PI Tessier-Lavigne M, Leonardo ED, Hinck L, Masu M, Keinomasu K;

XX

DR P-PSDB; AAW78898.

XX

PT Netrin-binding, vertebrate proteins - useful for diagnosis, therapy and  
PT the biopharmaceutical industry.

XX

PS Claim 7; Page 15-17; 32pp; English.

XX

CC This cDNA, termed unc5h-1, comprises a rat homologue of *Caenorhabditis*  
CC *elegans* unc-5. Rat unc5h-1 and unc5h-2 (see AAV52942) cDNAs were isolated  
CC from an E18 brain cDNA library. The predicted proteins (see AAW78898 and  
CC AAW78900) show similarity with UNC-5. They are predicted to be involved  
CC in cell migration and axon guidance, and are characterised as receptor  
CC proteins for netrins. Gene expression is observed in regions where  
CC differentiating neurons are undergoing axogenesis. Human unc5h-1 (see  
CC AAV52941) and unc5h-2 (see AAV52943) cDNAs are also claimed. Vertebrate  
CC UNC-5 proteins may be produced recombinantly from transfected host cells  
CC by utilising these vertebrate UNC-5 nucleic acids. The invention also  
CC provides unc-5 hybridisation probes and primers, vertebrate UNC-5-  
CC specific binding agents such as specific antibodies, and methods of  
CC making and using the subject compositions in diagnosis (e.g. genetic  
CC hybridisation screens for vertebrate unc-5 transcripts), therapy (e.g.  
CC gene therapy to modulate vertebrate unc-5 gene expression) and in the  
CC biopharmaceutical industry (e.g. as immunogens, reagents for modulating  
CC cell guidance, reagents for screening chemical libraries for lead  
CC pharmacological agents, etc.). (Updated on 25-MAR-2003 to correct PI  
CC field.)

XX

SQ Sequence 3014 BP; 596 A; 977 C; 849 G; 592 T; 0 U; 0 Other;

Query Match 82.1%; Score 2259; DB 2; Length 3014;  
Best Local Similarity 89.7%; Pred. No. 0;  
Matches 2427; Conservative 0; Mismatches 280; Indels 0; Gaps 0;

Qy	46	ATGGCCGTCCGGCCCGGCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTC	105
Db	1	ATGGCCGTCCGGCCCGGCTGTGGCCAGTGCTCCTGGGCATAGTCCTCGCCGCTTGGCTT	60
Qy	106	CGCGGCTCGGGTGCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCG	165
Db	61	CGTGGTTCGGGTGCCAGCAGAGTGCCACGGTGGCCAATCCAGTGCCCGGTGCCAACCCC	120
Qy	166	GACCTGCTTCCCCACTTCTTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCA	225
Db	121	GACCTGCTGCCCCACTTCTTGGTAGAGCCTGAGGACGTGTACATTGTCAAGAACAAGCCG	180
Qy	226	GTGCTGCTTGTGTGCAAGGCCGTGCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAG	285
Db	181	GTGTTGTTGGTGTGCAAGGCTGTGCCTGCCACCCAGATCTTCTTCAAGTGCAATGGGGAA	240
Qy	286	TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCC	345
Db	241	TGGGTCCGCCAGGTGCATCACGTAATTGAACGCAGCACCGACAGCAGCAGCGGATTGCCA	300
Qy	346	ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTTCGAGAAGGTGTTCCGGGCTGGAG	405
Db	301	ACCATGGAGGTCCGTATCAACGTATCGAGGCAGCAGGTAGAGAAAAGTGTTTGGGCTGGAG	360

Qy	406	GAATACTGGTGCCAGTGCCTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC	465
Db	361	GAATACTGGTGCCAGTGTGTGGCATGGAGCTCCTCGGGTACCACCAAAAGTCAGAAGGCC	420
Qy	466	TACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG	525
Db	421	TACATCCGGATTGCCTATTTGCGCAAGAACTTTGAGCAGGAGCCACTGGCCAAGGAAGTG	480
Qy	526	TCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGAGGGCATCCCTCCAGCCGAG	585
Db	481	TCACTGGAGCAAGGCATTGTACTACCTTGTCGCCCCCAGAAGGAATCCCCCAGCTGAG	540
Qy	586	GTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATC	645
Db	541	GTGGAGTGGCTTCGAAATGAGGACCTCGTGGACCCCTCCCTCGATCCCAATGTGTACATC	600
Qy	646	ACGCGGGAGCACAGCCTGGTGGTGCAGACAGGCCCGCCTTGCTGACACGGCCAACTACACC	705
Db	601	ACGCGGGAGCACAGCCTAGTCGTGCGTCAGGCCCGCCTGGCCGACACGGCCAACTACACC	660
Qy	706	TGCGTGGCCAAGAACATCGTGGCACGTTCGCCGAGCGCCTCCGCTGCTGTCATCGTCTAC	765
Db	661	TGTGTGGCCAAGAACATCGTAGCCCGTCGCCGAAGCACCTCTGCAGCGGTCAATTGTTTAT	720
Qy	766	GTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGC	825
Db	721	GTGAACGGTGGGTGGTTCGACGTGGACTGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGT	780
Qy	826	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTC	885
Db	781	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCACCTCTCAACGGGGGCGCCTTC	840
Qy	886	TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGC	945
Db	841	TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACTCTGTGCCCAGTGGATGGGAGC	900
Qy	946	TGGAGCCCGTGGAGCAAGTGGTTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGT	1005
Db	901	TGGAGTTCGTGGAGTAAGTGGTTCAGCCTGTGGGCTTGACTGCACCCACTGGCGGAGCCGC	960
Qy	1006	GAGTGTCTTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGAC	1065
Db	961	GAGTGTCTTGACCCAGCACCCCGCAATGGAGGTGAGGAGTGTGCGGGTGTGACCTGGAC	1020
Qy	1066	ACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCC	1125
Db	1021	ACCCGCAACTGTACCAGTGACCTCTGCCTGCACACCGCTTCTTGCCCCGAGGACGTGGCT	1080
Qy	1126	CTCTATGTGGGCCCTCATCGCCGTGGCCGTCTGCCTGGTCTCTGCTGCTGCTTGTCTCATC	1185
Db	1081	CTCTACATCGGCCTTGTGCTGTGGCTGTGTGCCTCTTCTTGCTGTTGCTGGCCCTTGGA	1140
Qy	1186	CTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTC	1245
Db	1141	CTCATTTACTGTCGCAAGAAGGAAGGGCTGGACTCCGATGTGGCCGACTCGTCCATCCTC	1200

Qy	1246	ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTC	1305
Db	1201	ACCTCGGGCTTCCAGCCTGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCACCTGCTC	1260
Qy	1306	ACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG	1365
Db	1261	ACCATCCAGCCAGACCTCAGCACCACCACCTACCACCTACCAGGGCAGTCTATGTTTCGAGG	1320
Qy	1366	CAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGT	1425
Db	1321	CAGGATGGACCCAGCCCCAAGTTCCAGCTCTCTAATGGTCACCTGCTCAGCCCACCTGGGG	1380
Qy	1426	GGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCC	1485
Db	1381	AGTGGCCGCCATACGTTGCACCACAGCTCACCCACCTCTGAGGCTGAGGACTTCGTCTCC	1440
Qy	1486	CGCCTCTCCACCCAGAATACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTAT	1545
Db	1441	CGCCTCTCCACCCAAAATACTTTCGTTCCCTGCCCCGCGGCACCAGCAACATGGCCTAC	1500
Qy	1546	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTC	1605
Db	1501	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACGGGGATCAGCCTCCTC	1560
Qy	1606	ATCCCCCAGATGCCATACCCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG	1665
Db	1561	ATACCCCCGGATGCCATCCCCCGAGGAAAGATCTACGAGATCTACCTCACACTGCACAAG	1620
Qy	1666	CCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGC	1725
Db	1621	CCAGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCAGTCGTTAGC	1680
Qy	1726	TGTGGACCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGG	1785
Db	1681	TGTGGGCCCCCAGGAGTCCTGCTCACCCGGCCAGTCATCCTTGCAATGGACCACTGTGGA	1740
Qy	1786	GAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG	1845
Db	1741	GAGCCCAGCCCTGACAGCTGGAGTCTGCGCCTCAAAAAGCAGTCCTGCGAGGGCAGTTGG	1800
Qy	1846	GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAG	1905
Db	1801	GAGGATGTGCTGCACCTTGGTGAGGAGTCACCTTCCACCTCTACTACTGCCAGCTGGAG	1860
Qy	1906	GCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCC	1965
Db	1861	GCCGGGGCCTGCTATGTCTTCACGGAGCAGCTGGGCCGCTTTGCCCTGGTAGGAGAGGCC	1920
Qy	1966	CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC	2025
Db	1921	CTCAGCGTGGCTGCCACCAAGCGCCTCAGGCTCCTTCTGTTTGCTCCCGTGGCCTGTACG	1980
Qy	2026	TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG	2085
Db	1981	TCCCTTGAGTACAACATCCGAGTGTACTGCCTACACGACACCCACGACGCTCTCAAGGAG	2040
Qy	2086	GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCAC	2145



Db	2041	 GTGGTGCAGCTGGAGAAGCAGCTAGGTGGACAGCTGATCCAGGAGCCTCGCGTCCTGCAC	2100
Qy	2146	TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGG	2205
Db	2101	TTCAAAGACAGTTACCACAACCTACGTCTCTCCATCCACGACGTGCCAGCTCCCTGTGG	2160
Qy	2206	AAGAGTAAGCTCCTTGTCTAGCTACCAGGAGATCCCTTTTATCACATCTGGAATGGCAGC	2265
Db	2161	AAGAGCAAGCTACTTGTCTAGCTACCAGGAGATCCCTTTTACCACATCTGGAACGGCACC	2220
Qy	2266	CAGCGGTACTTGCCTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTG	2325
Db	2221	CAGCAGTATCTGCCTGCACCTTCACCCTGGAGCGCATCAACGCCAGCACCAGCGACCTG	2280
Qy	2326	GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTC	2385
Db	2281	GCCTGCAAGGTGTGGGTGTGGCAGGTGGAGGGAGATGGGCAGAGCTTCAACATCAACTTC	2340
Qy	2386	AACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTC	2445
Db	2341	AACATCACTAAGGACACAAGGTTTGCTGAATTGTTGGCTCTGGAGAGTGAAGGGGGGGTC	2400
Qy	2446	CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATT	2505
Db	2401	CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAAAAGATCATC	2460
Qy	2506	TCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTC	2565
Db	2461	GCCAGTCTGGACCCACCCTGCAGCCGGGGCGCCGACTGGAGAACTCTAGCCCAGAACTT	2520
Qy	2566	CACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTC	2625
Db	2521	CACCTGGACAGCCATCTTAGCTTCTTTGCCTCCAAGCCCAGCCCTACAGCCATGATCCTC	2580
Qy	2626	AACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTG	2685
Db	2581	AACCTATGGGAGGCACGGCACTTCCCCAACGGCAACCTCGGCCAGCTGGCAGCAGCTGTG	2640
Qy	2686	GCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTGCGGAGGCTGAGTGCTGAGGC	2745
Db	2641	GCCGGACTGGGCCAACCAGATGCTGGCCTCTTCACGGTGTGCGGAGGCCGAGTGTTGAGAC	2700
Qy	2746	CGGCCAG	2752
Db	2701	CAGCCAG	2707

RESULT 7  
 AAS16843  
 ID AAS16843 standard; cDNA; 2697 BP.  
 XX  
 AC AAS16843;  
 XX  
 DT 14-FEB-2002 (first entry)  
 XX  
 DE Rat netrin receptor UNC5H1 (YSG7) cDNA.

XX  
 KW YSG; YSG7; schizophrenia; chronic animal model; LCGU; netrin receptor;  
 KW local cerebral glucose utilisation; phosphodiesterase 1-alpha; UNC5H1;  
 KW calcium-independent alpha-latrotoxin receptor; CIRL; trkE; synapsin 1A;  
 KW epithelial discoidin domain receptor 1; synapsin 1B; neuroleptic; ss;  
 KW tumour necrosis factor alpha; TNF-alpha; rat.  
 XX  
 OS Rattus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1. .2697  
 FT /\*tag= a  
 FT /product= "Rat netrin receptor UNC5H1"  
 XX  
 PN WO200175440-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 02-APR-2001; 2001WO-GB001486.  
 XX  
 PR 31-MAR-2000; 2000GB-00007880.  
 PR 26-MAY-2000; 2000GB-00012768.  
 XX  
 PA (WELF-) WELFIDE CORP.  
 XX  
 PI Cochran S, Paterson G, Ohashi Y, Morris B, Pratt J;  
 XX  
 DR WPI; 2002-010813/01.  
 DR P-PSDB; AAU10543.  
 XX  
 PT Novel chronic animal model of schizophrenia, useful for identifying anti-  
 PT psychotic drugs and genes that are associated with schizophrenia.  
 XX  
 PS Claim 1; Fig 8a; 79pp; English.  
 XX  
 CC The invention relates to YSG polynucleotide fragments for use in  
 CC diagnosing and/or developing treatments for schizophrenia using chronic  
 CC animal models. The polynucleotides and their encoded polypeptides are  
 CC used for identification of compounds which modulate the expression of YSG  
 CC molecules, leading to the manufacture of schizophrenia medicaments. The  
 CC sequences can also be used for testing candidate compounds for any effect  
 CC on the polypeptides. Anti-schizophrenic effects of a compound can be  
 CC determined by measuring local cerebral glucose utilisation (LCGU) or  
 CC comparing its expression level with that of a control group. The  
 CC sequences are useful in the identification of genes associated with  
 CC schizophrenic states and in the development of an antibody. The sequences  
 CC of the invention include phosphodiesterase 1-alpha, calcium-independent  
 CC alpha-latrotoxin receptors (CIRL)-1,2&3, epithelial discoidin domain  
 CC receptor 1 (trkE), netrin receptor (UNC5H1), synapsins 1A and AB and  
 CC tumour necrosis factor (TNF) alpha. This sequence represents rat netrin  
 CC receptor UNC5H1 (YSG7) DNA  
 XX  
 SQ Sequence 2697 BP; 541 A; 864 C; 766 G; 526 T; 0 U; 0 Other;

Query Match 81.8%; Score 2252.2; DB 6; Length 2697;  
 Best Local Similarity 89.7%; Pred. No. 0;  
 Matches 2419; Conservative 0; Mismatches 278; Indels 0; Gaps 0;

Qy	46	ATGGCCGTCGGGCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTC	105
Db	1	ATGGCCGTCGGGCCCGGCCTGTGGCCAGTGCTCCTGGGCATAGTCCTCGCCGCTTGGCTT	60
Qy	106	CGCGGCTCGGGTGCCCAGCAGAGTGCCACCGTGCCCAACCCAGTGCTGGTGCCAACCCG	165
Db	61	CGTGGTTTCGGGTGCCAGCAGAGTGCCACGGTGCCCAATCCAGTGCCCGGTGCCAACCCC	120
Qy	166	GACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCA	225
Db	121	GACCTGCTGCCCCACTTCCTGGTAGAGCCTGAGGACGTGTACATTGTCAAGAACAAGCCG	180
Qy	226	GTGCTGCTTGTGTGCAAGGCCGTGCCC GCCACGCAGATCTTCTTCAAGTGCAACGGGGAG	285
Db	181	GTGTTGTTGGTGTGCAAGGCTGTGCCTGCCACCCAGATCTTCTTCAAGTGCAATGGGGAA	240
Qy	286	TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCC	345
Db	241	TGGGTCCGCCAGGTCGATCACGTAATTGAACGCAGCACCGACAGCAGCAGCGGATTGCCA	300
Qy	346	ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTGCGGCTGGAG	405
Db	301	ACCATGGAGGTCCGTATCAACGTATCGAGGCAGCAGGTAGAGAAAGTGTGTTGGGCTGGAG	360
Qy	406	GAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC	465
Db	361	GAATACTGGTGCCAGTGTTGTGGCATGGAGCTCCTCGGGTACCACCAAAAGTCAGAAGGCC	420
Qy	466	TACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG	525
Db	421	TACATCCGGATTGCCTATTTGCGCAAGAACTTTGAGCAGGAGCCACTGGCCAAGGAAGTG	480
Qy	526	TCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGGCATCCCTCCAGCCGAG	585
Db	481	TCACTGGAGCAAGGCATTGTACTACCTTGTGCCCCCAGAAGGAATCCCCCAGCTGAG	540
Qy	586	GTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATC	645
Db	541	GTGGAGTGGCTTCGAAATGAGGACCTCGTGGACCCCTCCCTCGATCCCAATGTGTACATC	600
Qy	646	ACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACC	705
Db	601	ACGCGGGAGCACAGCCTAGTCGTGCGTCAGGCCCGCCTGGCCGACACGGCCAACTACACC	660
Qy	706	TGCGTGGCCAAGAACATCGTGGCACGTGCGCCGACGCGCTCCGCTGCTGTCATCGTCTAC	765
Db	661	TGTGTGGCCAAGAACATCGTAGCCCGTCGCCGAAGCACCTCTGCAGCGGTCAATTGTTTAT	720
Qy	766	GTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGC	825
Db	721	GTGAACGGTGGGTGGTTCGACGTGGACTGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGT	780
Qy	826	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGCGCTTTC	885
Db	781	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCACCTCTCAACGGGGCGCCTTTC	840

Qy 886 TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGC 945  
 Db 841 TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACTCTGTGCCCAGTGGATGGGAGC 900

Qy 946 TGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGT 1005  
 Db 901 TGGAGTTCGTGGAGTAAGTGGTCAGCCTGTGGGCTTGAAGTGCACCCACTGGCGGAGCCGC 960

Qy 1006 GAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGAC 1065  
 Db 961 GAGTGCTCTGACCCAGCACCCCGCAATGGAGGTGAGGAGTGTGCGGGTGTGACCTGGAC 1020

Qy 1066 ACCCGCAACTGTACCACTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCC 1125  
 Db 1021 ACCCGCAACTGTACCACTGACCTCTGCCTGCACACCGCTTCTTGCCCCGAGGACGTGGCT 1080

Qy 1126 CTCTATGTGGGCTCATCGCCGTGGCCGTCTGCCTGGTCTGCTGCTGCTTGTCTCATC 1185  
 Db 1081 CTCTACATCGGCCTTGTGCTGTGGCTGTGTGCCTCTTCTTGCTGTTGCTGGCCCTTGA 1140

Qy 1186 CTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTC 1245  
 Db 1141 CTCATTTACTGTGCAAGAAGGAAGGGCTGGACTCCGATGTGGCCGACTCGTCCATCCTC 1200

Qy 1246 ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCATCTGCTC 1305  
 Db 1201 ACCTCGGGCTTCCAGCCTGTGAGCATCAAGCCCAGCAAAGCAGACAACCCCATCTGCTC 1260

Qy 1306 ACCATCCAGCCGGACCTCAGCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG 1365  
 Db 1261 ACCATCCAGCCGACCTCAGCACCACCACCACCTACCAGGGCAGTCTATGTTGAGG 1320

Qy 1366 CAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGT 1425  
 Db 1321 CAGGATGGACCCAGCCCCAAGTTCCAGCTCTCTAATGGTCACCTGCTCAGCCACTGGGG 1380

Qy 1426 GGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCC 1485  
 Db 1381 AGTGCCGCCCATACGTTGCACCACAGCTCACCCACCTCTGAGGCTGAGGACTTCGTCTCC 1440

Qy 1486 CGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTAT 1545  
 Db 1441 CGCCTCTCCACCCAAACTACTTTTCGTTCCCTGCCCCGCGGCACCAGCAACATGGCCTAC 1500

Qy 1546 GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTC 1605  
 Db 1501 GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACGGGGATCAGCCTCCTC 1560

Qy 1606 ATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG 1665  
 Db 1561 ATACCCCGGATGCCATACCCCGAGGAAAGATCTACGAGATCTACCTCACACTGCACAAG 1620

Qy 1666 CCGGAAGACGTGAGGTTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGC 1725  
 Db 1621 CCAGAAGACGTGAGGTTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCAGTCGTTAGC 1680

Qy 1726 TGTGGACCCCTGGCGTCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGG 1785

Db	1681	TGTGGGCCCCCAGGAGTCCTGCTCACCCGGCCAGTCATCCTTGCAATGGACCACTGTGGA	1740
Qy	1786	GAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG	1845
Db	1741	GAGCCCAGCCCTGACAGCTGGAGTCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGTTGG	1800
Qy	1846	GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAG	1905
Db	1801	GAGGATGTGCTGCACCTTGGTGAGGAGTCACCTTCCCACCTCTACTACTGCCAGCTGGAG	1860
Qy	1906	GCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCC	1965
Db	1861	GCCGGGGCCTGCTATGTCTTCACGGAGCAGCTGGGCCGCTTTGCCCTGGTAGGAGAGGCC	1920
Qy	1966	CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC	2025
Db	1921	CTCAGCGTGGCTGCCACCAAGCGCCTCAGGCTCCTTCTGTTTGCCTCCCGTGGCCTGTACG	1980
Qy	2026	TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG	2085
Db	1981	TCCCTTGAGTACAACATCCGAGTGTACTGCCTACACGACACCCACGACGCTCTCAAGGAG	2040
Qy	2086	GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCAC	2145
Db	2041	GTGGTGCAGCTGGAGAAGCAGCTAGGTGGACAGCTGATCCAGGAGCCTCGCGTCTGCAC	2100
Qy	2146	TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGG	2205
Db	2101	TTCAAAGACAGTTACCACAACCTACGTCTCTCCATCCACGAGCTGCCAGCTCCCTGTGG	2160
Qy	2206	AAGAGTAAGCTCCTTGTGCTAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCAG	2265
Db	2161	AAGAGCAAGCTACTTGTGCTAGCTACCAGGAGATCCCCTTTTACCACATCTGGAACGGCACC	2220
Qy	2266	CAGCGGTACTTGCCTGCACCTTACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTG	2325
Db	2221	CAGCAGTATCTGCCTGCACCTTACCCTGGAGCGCATCAACGCCAGCACCAGCGACCTG	2280
Qy	2326	GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTC	2385
Db	2281	GCCTGCAAGGTGTGGGTGTGGCAGGTGGAGGGAGATGGGCAGAGCTTCAACATCAACTTC	2340
Qy	2386	AACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTTC	2445
Db	2341	AACATCACTAAGGACACAAGGTTTGCTGAATTGTTGGCTCTGGAGAGTGAAGGGGGGGTTC	2400
Qy	2446	CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTGGCAGAAGATAATT	2505
Db	2401	CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTGGGAAAAGATCATC	2460
Qy	2506	TCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTC	2565
Db	2461	GCCAGTCTGGACCCACCCTGCAGCCGGGGCGCCGACTGGAGAAGTCTAGCCCAGAACTT	2520
Qy	2566	CACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTC	2625

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Db      2521 CACCTGGACAGCCATCTTAGCTTCTTTGCCTCCAAGCCCAGCCCTACAGCCATGATCCTC 2580
Qy      2626 AACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTG 2685
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      2581 AACCTATGGGAGGCACGGCACTTCCCCAACGGCAACCTCGGCCAGCTGGCAGCAGCTGTG 2640
Qy      2686 GCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGA 2742
        || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      2641 GCCGGACTGGGCCAACCAGATGCTGGCCTCTTCACGGTGTCTGGAGGCCGAGTGTTGA 2697

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RESULT 8

AAV52941

ID AAV52941 standard; cDNA; 1787 BP.

XX

AC AAV52941;

XX

DT 25-MAR-2003 (revised)

DT 21-DEC-1998 (first entry)

XX

DE Human UNC-5 homologue unc5h-1 cDNA.

XX

KW UNC-5; UNC5H-1; human; netrin receptor; cell migration; axon guidance;  
 KW diagnosis; therapy; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 3. .1670

FT /\*tag= a

FT /transl\_except= (pos:21. .22, aa:Xaa)

FT /transl\_except= (pos:200. .203, aa:Ile)

FT /transl\_except= (pos:771. .772, aa:Ser)

FT /transl\_except= (pos:785. .786, aa:Leu)

FT /transl\_except= (pos:1078. .1079, aa:Xaa)

FT /transl\_except= (pos:1098. .1099, aa:Xaa)

FT /transl\_except= (pos:1106. .1107, aa:Xaa)

FT /transl\_except= (pos:1621. .1622, aa:Gly)

FT /note= "these codons have apparent 1 nucleotide deletions  
 FT or insertions, which alter the reading frame"

XX

PN WO9837085-A1.

XX

PD 27-AUG-1998.

XX

PF 19-FEB-1998; 98WO-US003143.

XX

PR 19-FEB-1997; 97US-00808982.

XX

PA (REGC ) UNIV CALIFORNIA.

XX

PI Tessier-Lavigne M, Leonardo ED, Hinck L, Masu M, Keinomasu K;

XX

DR WPI; 1998-495364/42.

DR P-PSDB; AAW78899.

XX

PT Netrin-binding, vertebrate proteins - useful for diagnosis, therapy and



Qy	1489	CTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGG	1548
Db	420	CTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGG	479
Qy	1549	ACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATC	1608
Db	480	ACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGAATCAGCCTCCTCATC	539
Qy	1609	CCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCG	1668
Db	540	CCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCG	599
Qy	1669	GAAGACGTGAGGTTGCCCTAGCTGGCTGTGACACCCTGCTGAGTCCCATCGTTAGCTGT	1728
Db	600	GAAGACGTGAGGTTGCCCTAGCTGGCTGTGACACCCTGCTGAGTCCCATCGTTAGCTGT	659
Qy	1729	GGACCCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCAC'TGTGGGGAG	1788
Db	660	GGACCCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCAC'TGTGGGGAG	719
Qy	1789	CCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAG	1848
Db	720	CCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGG-AGCTGGGAG	778
Qy	1849	GATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCC	1908
Db	779	GATGT-CTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCC	837
Qy	1909	AGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCGCCTTTGCCCTGGTGGGAGAGGCCCTC	1968
Db	838	AGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCGCCTTTGCCCTGGTGGGAGAGGCCCTC	897
Qy	1969	AGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCC	2028
Db	898	AGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCC	957
Qy	2029	CTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTG	2088
Db	958	CTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTG	1017
Qy	2089	GTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACCTT	2148
Db	1018	GTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACCT-	1076
Qy	2149	AAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAG	2208
Db	1077	AAGGACAGTTACCACAACCT--GCCCTATCATCCACGATGTGCCCAGCTCCCTGTGGAAG	1134
Qy	2209	AGTAAGCTCCTTGTGTCAGTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAG	2268
Db	1135	AGTAAGCTCCTTGTGTCAGTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAG	1194
Qy	2269	CGGTACTTGCACTGCACCTTACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCC	2328
Db	1195	CGGTACTTGCACTGCACCTTACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCC	1254



Qy	2329	TGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAAC	2388
Db	1255	TGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAAC	1314
Qy	2389	ATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGTCCCA	2448
Db	1315	ATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGTCCCA	1374
Qy	2449	GCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCCTTCCTCATTCGGCAGAAGATAATTTCC	2508
Db	1375	GCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCCTTCCTCATTCGGCAGAAGATAATTTCC	1434
Qy	2509	AGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCAC	2568
Db	1435	AGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCAC	1494
Qy	2569	CTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAAC	2628
Db	1495	CTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAAC	1554
Qy	2629	CTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCT	2688
Db	1555	CTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCT	1614
Qy	2689	GGACTGGGCCAGCCAGACGCTGGCCTC-TTCACAGTG-TCGGAGGCTGAGTGCTGAGGCC	2746
Db	1615	GGGACTGGCCAGCAGGACGGTGGCTTCTTTACAGTGTTTCGGAGGCTGAGTGCTGAGGCC	1674
Qy	2747	GGCCAG 2752	
Db	1675	GGCCAG 1680	

# RESULT 9

AAC90958

ID AAC90958 standard; cDNA; 9700 BP.

XX

AC AAC90958;

XX

DT 19-MAR-2001 (first entry)

XX

DE Plasmid pGC1037 nucleotide sequence SEQ ID NO:91.

XX

KW Human; Caenorhabditis elegans; UNC-5; splice variant; nematode worm;

KW protein-protein interaction; identification; ss.

XX

OS Synthetic.

XX

PN WO200073328-A2.

XX

PD 07-DEC-2000.

XX

PF 02-JUN-2000; 2000WO-EP005108.

XX

PR 01-JUN-1999; 99GB-00012755.

XX

PA (DEVG-) DEVGEN NV.

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XX
PI Van Crielinge W, Roelens I, Bogaert T, Verwaerde P;
XX
DR WPI; 2001-016508/02.
XX
PT Three variants of human unc-5C cDNAs (unc-5Cb, unc-5Cc and unc-5C8) and a
PT human unc-5HS1 cDNA, useful in yeast two hybrid experiments for
PT identifying unknown human cDNAs which encode proteins that interact with
PT the human unc-5C protein.
XX
PS Example 4; Page 228-230; 246pp; English.
XX
CC The present invention describes 3 variants of human unc-5C cDNAs (unc-
CC 5Cb, unc-5Cc and unc-5C8) which correspond to alternatively spliced unc-
CC 5C transcripts, and a human unc-5HS1 cDNA which shares homology with the
CC Rattus norvegicus unc-5HS1 cDNA. Also described are assays based on
CC protein-protein-interactions between the unc-5 protein and a variety of
CC different interacting proteins. The unc-5C variant cDNAs and unc-5HS1
CC cDNA are useful in methods for identifying compounds which reduce or
CC inhibit the lethal phenotype associated with the expression of the unc-5
CC death domain in yeast. They are also useful in yeast two hybrid
CC experiments for identifying unknown human cDNAs which encode proteins
CC that interact with the human unc-5C protein. AAC90914 to AAC90971 and
CC AAB50646 to AAB50693 represent sequences used in the exemplification of
CC the present invention
XX
SQ Sequence 9700 BP; 2604 A; 2193 C; 2236 G; 2666 T; 0 U; 1 Other;

Query Match          47.4%; Score 1304.2; DB 4; Length 9700;
Best Local Similarity 99.8%; Pred. No. 2.1e-242;
Matches 1306; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1437 CACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCAC 1496
      |||
Db      7 CACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCAC 66

Qy      1497 CCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAA 1556
      |||
Db      67 CCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAA 126

Qy      1557 CTTCTCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGA 1616
      |||
Db      127 CTTCTCTCGGGGGCCGGCTGATGATCCCTAATACAGGAATCAGCCTCCTCATCCCCCAGA 186

Qy      1617 TGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGT 1676
      |||
Db      187 TGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGT 246

Qy      1677 GAGGTTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCC 1736
      |||
Db      247 GAGGTTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCC 306

Qy      1737 TGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCC 1796
      |||
Db      307 TGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCC 366

Qy      1797 TGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGGAGCTGGGAGGATGTGCT 1856

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Db	367	 TGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCT	426
Qy	1857	GCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTG	1916
Db	427	 GCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTG	486
Qy	1917	CTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGC	1976
Db	487	 CTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGC	546
Qy	1977	TGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTA	2036
Db	547	 TGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTA	606
Qy	2037	CAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCT	2096
Db	607	 CAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCT	666
Qy	2097	GGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGACAG	2156
Db	667	 GGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGACAG	726
Qy	2157	TTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCT	2216
Db	727	 TTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCT	786
Qy	2217	CCTTGTGTCAGCTACCAGGAGATCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTT	2276
Db	787	 CCTTGTGTCAGCTACCAGGAGATCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTT	846
Qy	2277	GCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCT	2336
Db	847	 GCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCT	906
Qy	2337	GTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAA	2396
Db	907	 GTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAA	966
Qy	2397	GGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGT	2456
Db	967	 GGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCAAGCCCTGGT	1026
Qy	2457	GGGCCCCAGTGCCTTCAAGATCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGA	2516
Db	1027	 GGGCCCCAGTGCCTTCAAGATCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGA	1086
Qy	2517	CCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAG	2576
Db	1087	 CCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAG	1146
Qy	2577	CCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGA	2636
Db	1147	 CCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGA	1206
Qy	2637	GGCGCGGCACCTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGG	2696

Db 1207 GGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGG 1266

Qy 2697 CCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGAGGC 2745  
 ||| |

Db 1267 CCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGAGTC 1315

RESULT 10

AAH99530

ID AAH99530 standard; cDNA; 1321 BP.

XX

AC AAH99530;

XX

DT 16-OCT-2001 (first entry)

XX

DE Human protein encoding cDNA sequence SEQ ID NO:365.

XX

KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;  
 KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;  
 KW antibacterial; endocrine; cardiant; central nervous system; virucide;  
 KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;  
 KW antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;  
 KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;  
 KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;  
 KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;  
 KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;  
 KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;  
 KW genetic disease; haematopoietic disorder; platelet disorder; asthma;  
 KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;  
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;  
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;  
 KW neurological disorder; ss.

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OS Homo sapiens.

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PN WO200153455-A2.

XX

PD 26-JUL-2001.

XX

PF 22-DEC-2000; 2000WO-US035017.

XX

PR 23-DEC-1999; 99US-00471275.

PR 21-JAN-2000; 2000US-00488725.

PR 25-APR-2000; 2000US-00552317.

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PA (HYSE-) HYSEQ INC.

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PI Tang YT, Liu C, Drmanac RT;

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DR WPI; 2001-457603/49.

DR P-PSDB; AAM25589.

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PT Isolated human polynucleotides encoding polypeptides, useful for the  
 PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection.

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PS Claim 1; Page 471; 1217pp; English.

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CC AAH99166 to AAH99904 encode the human proteins given in AAM25225 to  
 CC AAM25963. The proteins can have activities based on the tissues and cells  
 CC they are expressed in, such as: antiinflammatory; antirheumatic;  
 CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;  
 CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;  
 CC cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary;  
 CC antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic;  
 CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;  
 CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides  
 CC encoding them can be used in gene therapy, antisense therapy and vaccine  
 CC production, The proteins and polynucleotides are useful for screening for  
 CC agonists or antagonists of a protein and for the treatment and diagnosis  
 CC of disorders associated with the activity of a protein e.g. inflammation,  
 CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,  
 CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal  
 CC infections, autoimmunity, genetic diseases, haematopoietic disorders,  
 CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,  
 CC osteoporosis, severe combined immunodeficiency, eczema, allergic  
 CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,  
 CC Alzheimer's disease, Parkinson's disease, neurodegenerative and  
 CC neurological disorders

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SQ Sequence 1321 BP; 258 A; 440 C; 371 G; 252 T; 0 U; 0 Other;

Query Match 43.8%; Score 1206.6; DB 4; Length 1321;  
 Best Local Similarity 98.0%; Pred. No. 1.1e-223;  
 Matches 1295; Conservative 0; Mismatches 19; Indels 7; Gaps 7;

Qy	1435	CACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCC	1494
Db	1	CACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCC	60
Qy	1495	ACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTC	1554
Db	61	ACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTC	120
Qy	1555	AACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCA	1614
Db	121	AACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGAATCAGCCTCCTCATCCCCCA	180
Qy	1615	GATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGAC	1674
Db	181	GATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGAC	240
Qy	1675	GTGAGGTTGCCCTTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCC	1734
Db	241	GTGAGGTTGCCCTTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCC	300
Qy	1735	CCT-GGCGTCCTGCTCACCCGGCCAGTCATCCT-GGCTATGGACCACTGT-GGGGAGCCC	1791
Db	301	CCTGGGCGTCCTGCTTACCCGGCCAGTCATCCTGGGGTATGGACCACTGTGGGGGAGCCC	360
Qy	1792	AGCCCTGACAGCT-GGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGA	1850
Db	361	AGCCCTGACAGCTGGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGA	420
Qy	1851	TGTGCTGCACCTGGGGCAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAG	1910

Db	421		TGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAG	480
Qy	1911		TGCCTGCTACGTCTTCACCGAGCAGCTGGGCGGCTTTGCCCTGGTGGGAGAGGCCCTCAG	1970
Db	481		TGCCTGCTACGTCTTCACCGAGCAGCTGAGCCGCTATGCCCTGGTGGGAGAGGCCCTCAG	540
Qy	1971		CGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCT	2030
Db	541		CGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCT	600
Qy	2031		CGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGT	2090
Db	601		CGAGTACAACATACTGGTCTACTGCCTGCATGACACTCACGATGCACTCAACGTAGTGGT	660
Qy	2091		GCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAA	2150
Db	661		GCAGCTGGAGAAGCAGCTGCAGGGACAGCTGATCCAGGAGCCACTGGTACTGCACTTCAA	720
Qy	2151		GGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAG	2210
Db	721		GGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAG	780
Qy	2211		TAAGCTCCTTGTCTAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCG	2270
Db	781		TAAGCTCCTTGTCTAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCG	840
Qy	2271		GTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTG	2330
Db	841		GTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTG	900
Qy	2331		CAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACAT	2390
Db	901		CAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACAT	960
Qy	2391		CACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGC	2450
Db	961		CACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGC	1020
Qy	2451		CCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAG	2510
Db	1021		CCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAG	1080
Qy	2511		CCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCT	2570
Db	1081		CCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCT	1140
Qy	2571		GGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCT	2630
Db	1141		GGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCT	1200
Qy	2631		GTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCT-G	2689
Db	1201		GTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGG	1260
Qy	2690		GACTGGGCCAGCCAGACGCTGGCCTC-TTCACAGTG-TCGGAGGCTGAGTGCTGAGGCCG	2747

Db 1261 GACTGGGCCAGCAGGACGGTGGCTTCTTTACAGTGTTCGGAGGCTGAGTGCTGAGGCCG 1320  
 Qy 2748 G 2748  
 |  
 Db 1321 G 1321

RESULT 11

AAS75738

ID AAS75738 standard; cDNA; 3646 BP.

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AC AAS75738;

XX

DT 13-FEB-2002 (first entry)

XX

DE DNA encoding novel human diagnostic protein #11542.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

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OS Homo sapiens.

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PN WO200175067-A2.

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PD 11-OCT-2001.

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PF 30-MAR-2001; 2001WO-US008631.

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PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

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PA (HYSE-) HYSEQ INC.

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PI Drmanac RT, Liu C, Tang YT;

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DR WPI; 2001-639362/73.

DR P-PSDB; ABG11551.

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PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.

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PS Claim 1; SEQ ID NO 11542; 103pp; English.

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CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The

CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
CC coding sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 3646 BP; 930 A; 917 C; 921 G; 877 T; 0 U; 1 Other;

Query Match 35.2%; Score 970; DB 5; Length 3646;  
Best Local Similarity 61.3%; Pred. No. 6.6e-178;  
Matches 1680; Conservative 1; Mismatches 996; Indels 63; Gaps 5;

```
Qy      57  GCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGG 116
      || || ||      | | |||| || | | || | | | | | | | |
Db      220  GCTCGTGCTACCTGCCCTGGCCCTGCTCAGCGCCAGCGGCACTGGCTCCGCCGCCAAGA 279

Qy      117  TGCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCC 176
      || |      | | | | | | || | | | | | | | |
Db      280  TGATGACTTTTTTCATGAACTCCCAGAACTTTTCCTTCTGATCCACCTGAGCCTCTGCC 339

Qy      177  CCACTTCCTGGTGGAGCCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGTGCTTGT 236
      || |||| | |||| | || | | || | | |||| |||| || |
Db      340  ACATTTCCCTTATTGAGCCTGAAGAAGCTTATATTGTGAAGAATAAGCCTGTGAACCTGTA 399

Qy      237  GTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCA 296
      || || | | || |||| |||| || |||| || | | |||| | ||
Db      400  CTGTAAAGCAAGCCCTGCCACCCAGATCTATTTCAAGTGTAATAGTGAATGGGTTTCATCA 459

Qy      297  GGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCACCATGGAGGT 356
      | ||||| | | || | || || | | | | | | | | | || ||
Db      460  GAAGGACCACATAGTAGATGAAAGAGTAGATGAACTTCCGGTCTCATTGTCCGGGAAGT 519

Qy      357  CCGCATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTCCGGGCTGGAGGAATACTGGTG 416
      |||| | | || | |||| || || | | || | | | | |||||
Db      520  GAGCATTGAGATTTCCGCCAGCAAGTGGAAGAACTCTTTGGACCTGAAGATTACTGGTG 579

Qy      417  CCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCAT 476
      |||| | |||| |||| || || || || || | |||| | | ||||
Db      580  CCAGTGTGTGGCTGGAGCTCCGCGGGTACCACAAAGAGCCGGAAGGCGTATGTGCGCAT 639

Qy      477  AGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCA 536
      || | | || || |||| || |||| || || | |||| |||| || ||
Db      640  TGCATATCTACGGAAGACATTTGAGCAGGAACCCCTAGGAAAGGAAGTGTCTTTGGAACA 699

Qy      537  GGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCT 596
      || || | || | || || |||| || || |||| || |||| || ||
Db      700  GGAAGTCTTACTCCAGTGTGACACCTGAAGGGATCCCAGTGGCTGAGGTGGAATGGTT 759

Qy      597  CCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCA 656
      || || || | | || || || || || || || || || || || ||
Db      760  GAAAAATGAAGACATAATTGATCCCGTTGAAGATCGGAATTTTATATTACTATTGATCA 819

Qy      657  CAGCCTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACCTACACCTGCGTGGCCAA 716
```



Db 820 CAACCTCATCATAAAGCAGGCCCGACTCTCTGATACTGCAAATTACACCTGTGTTGCCAA 879  
 Qy 717 GAACATCGTGGCACGTGCGCCGAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGG 776  
 Db 880 AAACATTGTTGCCAAGAGGAAAAGTACAACTGCCACTGTCATAGTCTATGTCAACGGTGG 939  
 Qy 777 GTGGTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAA 836  
 Db 940 CTGGTCCACCTGGACGGAGTGGTCTGTGTGTAACAGCCGCTGTGGACGAGGGTATCAGAA 999  
 Qy 837 ACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCA 896  
 Db 1000 ACGTACAAGGACTTGTACCAACCCGGCACCCTCAATGGGGGTGCCTTCTGTGAAGGGCA 1059  
 Qy 897 GAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTG 956  
 Db 1060 GAGTGTGCAGAAAATAGCCTGTACTACGTTATGCCAGTGGATGGCAGGTGGACGCCATG 1119  
 Qy 957 GAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGA 1016  
 Db 1120 GAGCAAGTGGTCTACTTGTGAACTGAGTGCACCCACTGGCGCAGGAGGGAGTGCACGGC 1179  
 Qy 1017 CCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTG 1076  
 Db 1180 GCCAGCCCCCAAGAATGGAGGCAAGGACTGCGACGGCCTCGTCTTGCAATCCAAGAACTG 1239  
 Qy 1077 TACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGG 1136  
 Db 1240 CACTGATGGGCTTTGCATGCAGACTGCTCCTGATTAGATGATGTTGCTCTCTATGTTGG 1299  
 Qy 1137 ---CCTCATCGCCGTGGCCGTCTGCCTGGTCTCTGCTGCTTGTCTCATCCTCGTTTA 1193  
 Db 1300 GATTGTGATAGCAGTGATCGTTTGCCTGGCGATCTCTGTAGTTGTGGCCTTGTTTGTGTA 1359  
 Qy 1194 TTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGG 1253  
 Db 1360 TCGGAAGAATCATCGTGACTTTGAGTCAGATATTATTGACTCTTCGGCACTCAATGGGGG 1419  
 Qy 1254 CTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCA 1313  
 Db 1420 CTTTCARCTGTGAACATCAAG-----GCAGCAAGACAAGATCTGCTGGCTGTACC 1470  
 Qy 1314 GCCGGACCTCAGCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATG- 1372  
 Db 1471 CCCAGACCTCACGTGAGCTGCAGCCATGTACAGAGGACCTGTCTATGCCCTGCATGACGT 1530  
 Qy 1373 ----GGCCCAGCCCCAAGTTCAGCTACCAAT----GGGCACCTGCTCAGCCCCCTGGG 1424  
 Db 1531 CTCAGACAAAATCCCAATGACCAACTCTCCAATTCTGGATCCACTGCCCCAACCTGAAAAAT 1590  
 Qy 1425 TGGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTC 1484  
 Db 1591 CAAAGTGTACAACACCTCAGGTGCTGTCTCCCCCAAGATGACCTCTCTGAGTTTACGTC 1650  
 Qy 1485 CCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCGAGGCACCAGCAACATGA---- 1540

Db 1651 CAAGCTGTCCCCTCAGATGACCCAGTCGTTGTTGGAGAATGAAGCCCTCAGCCTGAAGAA 1710  
 Qy 1541 -----CCTATGGGACCTTCAACTTCCT 1562  
 | | | | | | | | | |  
 Db 1711 CCAGAGTCTAGCAAGGCAGACTGATCCATCCTGTACCGCATTGTCAGCTTCAACTCGCT 1770  
 Qy 1563 CGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCCAT 1622  
 | | | | | | | | | | | | | | | | | |  
 Db 1771 GGGAGGTCACCTTATTGTTCCCAATTCAGGAGTCAGCTTGCTGATTCCCGCTGGGGCCAT 1830  
 Qy 1623 ACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGGTT 1682  
 | | | | | | | | | | | | | | | | | |  
 Db 1831 TCCCCAAGGGAGAGTCTACGAAATGTATGTGACTGTACACAGGAAAGAACTATGAGGCC 1890  
 Qy 1683 GCCCCTAGCTGGCTGTGAGACCTGCTGAGTCCCATCGTTAGCTGTGGACCCCTGGCGT 1742  
 | | | | | | | | | | | | | | | | | |  
 Db 1891 ACCCATGGATGACTCTCAGACACTTTTGACCCCTGTGGTGAGCTGTGGGGCCCCAGGAGC 1950  
 Qy 1743 CCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGACAG 1802  
 | | | | | | | | | | | | | | | | | |  
 Db 1951 TCTGCTCACCCGCCCCGTCTGCTCACTATGCATCACTGCGCAGACCCCAATACCGAGGA 2010  
 Qy 1803 CTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCACCT 1862  
 | | | | | | | | | | | | | | | | | |  
 Db 2011 CTGGAAAATACTGCTCAAGAACCAGGCAGCACAGGGACAGTGGGAGGATGTGGTGGTGGT 2070  
 Qy 1863 GGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGT 1922  
 | | | | | | | | | | | | | | | | | |  
 Db 2071 CGGGGAGGAAAACCTTACCACCCCTGCTACATTAAGCTGGATGCAGAGGCCTGCCACAT 2130  
 Qy 1923 CTTACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGC 1982  
 | | | | | | | | | | | | | | | | | |  
 Db 2131 CCTCACAGAGAACCTCAGCACCTACGCCCTGGTAGGACATTCCACCACCAAAGCGGCTGC 2190  
 Qy 1983 CAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACAT 2042  
 | | | | | | | | | | | | | | | | | |  
 Db 2191 AAAGCGCCTCAAGCTGGCCATCTTTGGGCCCTGTGCTGCTCCTCGCTGGAGTACAGCAT 2250  
 Qy 2043 CCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAA 2102  
 | | | | | | | | | | | | | | | | | |  
 Db 2251 CCGAGTCTACTGTCTGGATGACACCCAGGATGCCCTGAAGGAAATTTTACATCTTGAGAG 2310  
 Qy 2103 GCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTCAAGGACAGTTACCA 2162  
 | | | | | | | | | | | | | | | | | |  
 Db 2311 ACAGACGGGAGGACAGCTCCTAGAAGAACCTAAGGCTCTTCATTTTAAAGGCAGCACCCA 2370  
 Qy 2163 CAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTTGT 2222  
 | | | | | | | | | | | | | | | | | |  
 Db 2371 CAACCTGCGCCTGTCAATTACGATATCGCCATTCCCTCTGGAAGAGCAAATTGCTGGC 2430  
 Qy 2223 CAGCTACCAGGAGATCCCCTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCACTG 2282  
 | | | | | | | | | | | | | | | | | |  
 Db 2431 TAAATATCAGGAAATTCATTTTACCATGTTTGGAGTGGATCTCAAAGAAACCTGCACTG 2490  
 Qy 2283 CACCTTCACCCTGGAGCGTGTGACCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGGGT 2342  
 | | | | | | | | | | | | | | | | | |  
 Db 2491 CACCTTCACTCTGGAAAGATTTAGCCTGAACACAGTGGAGCTGGTTTGCAAACCTCTGTGT 2550

Qy	2343	GTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAGGCAC	2402
Db	2551	GCGGCAGGTGGAAGGAGAAGGGCAGATCTTCCAGCTCAACTGCACCGTGTCTAGAGGAACC	2610
Qy	2403	AAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGTTGGGCCC	2462
Db	2611	TACTGGCATCGAATTTGCCGCTGCTGGATCCTGCGAACACCATCACCACGGTCACGGGGCC	2670
Qy	2463	CAGTGCCTTCAAGATCCCCTTCCTCATTGGCAGAAGATAATTTCCAGCCTGGACCCACC	2522
Db	2671	CAGTGCTTTTCAGCATCCCTCTCCCTATCCGGCAGAAGCTCTGTAGCAGCCTGGATGCCCC	2730
Qy	2523	CTGTAGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAGCCATCT	2582
Db	2731	CCAGACGAGAGGCCATGACTGGAGGATGCTGGCCCATAAGCTGAACCTGGACAGGTACTT	2790
Qy	2583	CAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCGCG	2642
Db	2791	GAATTACTTTGCCACCAAATCCAGCCCAACTGGCGTAATCCTGGATCTTTGGGAAGCACA	2850
Qy	2643	GCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAGCC	2702
Db	2851	GAACTTCCCAGATGGAACCTGAGCATGCTGGCAGCTGTCTTGGAAGAAATGGGAAGACA	2910
Qy	2703	AGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGA	2742
Db	2911	TGAAACGGTGGTGTCTTAGCAGCAGAAGGGCAGTATTAA	2950



Db 408 TGGAGGAGCTCTTTGGGCTGGAGGATTACTGGTGCCAGTGCGTGGCCTGGAGCTCCGCGG 467  
 Qy 443 GCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGC 502  
 ||||| ||||| ||||| ||| ||||| ||||| ||  
 Db 468 GCACCACCAAGAGTCGCCGAGCCTACGTCCGCATCGCCTACCTGCGCAAGAACTTCGATC 527  
 Qy 503 AGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCAC 562  
 ||||| ||||| ||||| ||||| ||| ||| ||||| |||  
 Db 528 AGGAGCCTCTGGGCAAGGAGGTGCCCCCTGGACCATGAGGTTCTCCTGCAGTGCCGCCCCG 587  
 Qy 563 CGGAGGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGT 622  
 ||||| ||| ||||| ||||| ||| ||||| ||| |||||  
 Db 588 CGGAGGGGGTGCCTGTGGCCGAGGTGGAATGGCTCAAGAATGAGGATGTCATCGACCCCA 647  
 Qy 623 CCCTGGACCCCAATGTATACATCACGCGGGAGCACAGCCTGGTGGTGGCAGAGCCCCGCC 682  
 ||| |||| |||| | |||| || |||| ||| | || |||||  
 Db 648 CCCAGGACACCAACTTCCTGCTCACCATCGACCACAACCTCATCATCCGCCAGGCCCCGCC 707  
 Qy 683 TTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAACATCGTGGCACGTGCGCCGAGCG 742  
 | | |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 708 TGTGCGGACACTGCCAACTATACCTGCGTGGCCAAGAACATCGTGGCCAAACGCCGGAGCA 767  
 Qy 743 CCTCCGCTGCTGTTCATCGTCTACGTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCG 802  
 || | || | ||||| ||||| || ||||| || ||||| || |||||  
 Db 768 CCACTGCCACCGTCATCGTCTACGTGAATGGCGGCTGGTCCAGCTGGGCAGAGTGGTCAC 827  
 Qy 803 TCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGG 862  
 |||| | | ||||| || ||||| ||||| || | ||||| ||||| |||||  
 Db 828 CCTGCTCCAACCGCTGTGGCCGAGGCTGGCAGAAGCGACCCGGACCTGCACCAACCCCG 887  
 Qy 863 CGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCGAATGTCCAGAAAACAGCCTGCGCCA 922  
 | || ||||| || || ||||| ||||| ||| ||||| || ||||| |||  
 Db 888 CTCCACTCAACGGAGGGGCGCTTCTGCGAGGGCCAGGCATTCCAGAAGACCGCCTGCACCA 947  
 Qy 923 CCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTCCGGCCTGTGGGCTGG 982  
 || | ||||| || || |||| ||||| ||||| ||||| ||| |  
 Db 948 CCATCTGCCCAGTCGATGGGGCGTGGACGGAGTGGAGCAAGTGGTCAGCCTGCAGCACTG 1007  
 Qy 983 ACTGCACCCACTGGCGGAGCCGTGAGTGTCTGACCCAGCACCCCGCAACGGAGGGGAGG 1042  
 | || ||||| ||||| ||||| | || ||||| ||||| |||  
 Db 1008 AGTGTGCCCACTGGCGTAGCCGCGAGTGCATGGCGCCCCACCCAGAACGGAGGCCGTG 1067  
 Qy 1043 AGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTG 1102  
 | ||| || || || |||| | |||| || || || || || ||  
 Db 1068 ACTGCAGCGGGACGCTGCTCGACTCTAAGAACTGCACAGATGGGCTGTGCATGCAACTGG 1127  
 Qy 1103 CTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGG 1162  
 | || || || || || || || || || || || || || ||  
 Db 1128 AGGCCTCAGGGGATGCGGCGCTGTATGCGGGGCTCGTGGTGGCCATCTTCGTGGTCTGG 1187  
 Qy 1163 TCCTGCTGCTGCTTGTCTCATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAG 1222  
 | || || || || || || || || || || || || || || ||  
 Db 1188 CAATCCTCATGGCGGTGGGGGTGGTGGTGTACCGCCGCAACTGCCGTGACTTCGACACAG 1247  
 Qy 1223 ATGTGGCTGACTCGTCCATT---CTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCA 1279  
 | | ||||| || | || || || |||| ||||| || || || ||  
 Db 1248 ACATCACTGACTCATCTGCTGCCCTGACTGGTGGTTTCCACCCCGTCAACTTTAAGACGG 1307

Qy 1280 GCAAAGCAGACAACCCCCATCTGCT-----CACCATCCAGCCGGACCTCAGCACCACCA 1333  
 | | | | | | | | | | | | | | | | | | |  
 Db 1308 CAAGGCCAGTAACCCGCAGCTCTACACCCCTCTGTGCCTCCTGACCTGACAGCCAGCG 1367

Qy 1334 CCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGA----- 1370  
 || || |||| | | | | | | | | | | | | |  
 Db 1368 CCGGCATCTACCGCGGACCCGTGTATGCCCTGCAGGACTCCACCGACAAAATCCCCATGA 1427

Qy 1371 -----TGGGCCAGCCCCAAGTTCCAGCTCACCA----- 1399  
 | | | | | | | | | | | | | | | | | | |  
 Db 1428 CCAACTCTCCTCTGCTGGACCCCTTACCAGCCTTAAGGTCAAGGTCTACAGCTCCAGCA 1487

Qy 1400 --ATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACAC-----ACTGCACC 1447  
 | | | | | | | | | | | | | | | | | | |  
 Db 1488 CCACGGGCTCTGGGCCAGGCCTGGCAGATGGGGCTGACCTGCTGGGGGTCTTGCCGCCTG 1547

Qy 1448 ACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAGAACTACT 1507  
 || | | | | | | | | | | | | | | | | | |  
 Db 1548 GCACATACCCTAGCGATTTCGCCCGGGACACCCACTTCCTGCACCTGCGCAGCGCCAGCC 1607

Qy 1508 TCCGCTC-----CCTGCCCGAGGCACCAGCAACATGACCTATGGGACCT 1552  
 || | | | | | | | | | | | | | | | | | |  
 Db 1608 TCGGTTCCCAGCAGCTCTTGGGCTGCCCGAGACCCAGGGAGCAGCGTCAGCGGCACCT 1667

Qy 1553 TCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCC 1612  
 | | | | | | | | | | | | | | | | | | |  
 Db 1668 TTGGCTGCCTGGGTGGGAGGCTCAGCATCCCCGGCACAGGGGTGAGCTTGCTGGTGCCCA 1727

Qy 1613 CAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAG 1672  
 | | | | | | | | | | | | | | | | | | |  
 Db 1728 ATGGAGCCATTCCCCAGGGCAAGTTCTACGAGATGTATCTACTCATCAACAAGGCAGAAA 1787

Qy 1673 ACGTGAGGTTGCCCCTAGCTGGCTGTGACCCCTGCTGAGTCCCATCGTTAGCTGTGGAC 1732  
 | | | | | | | | | | | | | | | | | | |  
 Db 1788 GTACCTTGCCGCTTTCAGAAGGGACCCAGACAGTATTGAGCCCCTCGGTGACCTGTGGAC 1847

Qy 1733 CCCCTGGCGTCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCA 1792  
 || | | | | | | | | | | | | | | | | | |  
 Db 1848 CCACAGGCCTCCTGCTGTGCCGCCCCGTATCCTCACCATGCCCCACTGTGCCGAAGTCA 1907

Qy 1793 GCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATG 1852  
 | | | | | | | | | | | | | | | | | | |  
 Db 1908 GTGCCCGTGACTGGATCTTTCAGCTCAAGACCCAGGCCCACCAGGGCCACTGGGAGGAGG 1967

Qy 1853 TGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTG 1912  
 || | | | | | | | | | | | | | | | | | |  
 Db 1968 TGGTGACCCTGGATGAGGAGACCCTGAACACACCCTGCTACTGCCAGCTGGAGCCCAGGG 2027

Qy 1913 CCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCG 1972  
 |||| | | | | | | | | | | | | | | | |  
 Db 2028 CCTGTCACATCCTGCTGGACCAGCTGGGCACCTACGTGTTACGGGCGAGTCCTATTCCC 2087

Qy 1973 TGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGGCGCCGGTGGCCTGCACCTCCCTCG 2032  
 | | | | | | | | | | | | | | | | | | |  
 Db 2088 GCTCAGCAGTCAAGCGGCTCCAGCTGGCCGTCTTCGCCCCCGCCCTCTGCACCTCCCTGG 2147



DE Human NOV1b coding sequence.  
 XX  
 KW Human; NOVX; autoimmune disease; cancer; infection; inflammatory disease;  
 KW storage disorder; muscle disorder; neurodegenerative disorder; nootropic;  
 KW developmental defect; neuroprotective; antiparkinsonian; hypotensive;  
 KW hypertensive; haemostatic; cardiant; antianginal; dermatological;  
 KW immunosuppressive; antiinflammatory; virucide; antibacterial; anti-HIV;  
 KW antiparasitic; antiallergic; antiasthmatic; antirheumatic; antiarthritic;  
 KW vulnerary; anorectic; antidiabetic; immunomodulator; antipsoriatic;  
 KW nephrotropic; kerolytic; antiulcer; cerebroprotective; anticonvulsant;  
 KW antiinfertility; antimanic; antidepressant; metabolic; cytostatic;  
 KW tranquilizer; analgesic; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200257450-A2.  
 XX  
 PD 25-JUL-2002.  
 XX  
 PF 29-NOV-2001; 2001WO-US048922.  
 XX  
 PR 29-NOV-2000; 2000US-0253834P.  
 PR 30-NOV-2000; 2000US-0250926P.  
 PR 25-JAN-2001; 2001US-0264180P.  
 PR 20-AUG-2001; 2001US-0313656P.  
 PR 05-OCT-2001; 2001US-0327456P.  
 PR 28-NOV-2001; 2001US-00327456.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Edinger S, Macdougall JR, Millet I, Ellerman K, Stone DJ;  
 PI Gerlach V, Grosse WM, Alsobrook JP, Lepley DM, Rieger D, Burgess CE;  
 PI Casman SJ, Spytek KA, Boldog FL, Li L, Padigar M, Mishra V;  
 PI Patturajan M, Shenoy S, Rastelli L, Tchernev VT, Vernet CAM;  
 PI Zerhusen BD, Malyankar UM, Guo X, Miller CE, Gangolli EA;  
 XX  
 DR WPI; 2002-590741/63.  
 DR P-PSDB; AAO18735.  
 XX  
 PT Novel isolated polypeptide, designated NOVX, useful for treating or  
 PT preventing in NOVX-associated disorders e.g. cardiomyopathy,  
 PT atherosclerosis, diabetes, cancer, allergy, asthma, Crohn's disease.  
 XX  
 PS Claim 9; Page 14; 353pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences of  
 CC several novel human proteins, designated NOVX. These can be used in the  
 CC treatment of, amongst others, cancers, autoimmune diseases, infections,  
 CC inflammatory diseases, storage disorders, muscle disorders,  
 CC neurodegenerative diseases and developmental defects. The present  
 CC sequence is a coding sequence of the invention  
 XX  
 SQ Sequence 2860 BP; 557 A; 950 C; 858 G; 495 T; 0 U; 0 Other;

Query Match 34.0%; Score 936.2; DB 6; Length 2860;  
 Best Local Similarity 61.7%; Pred. No. 2.2e-171;  
 Matches 1662; Conservative 0; Mismatches 938; Indels 93; Gaps 7;



Qy 143 ACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCCGAGGATG 202  
 || | | || | | | | | | | | | | | | | | | |  
 Db 168 ACTCCTTCCCGTCAGCGCCAGCAGAGCCGCTGCCCTACTTCCTGCAGGAGCCACAGGACG 227

Qy 203 TGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGCAAGGCCGTGCCCCGCCACGCAGA 262  
 |||| | | | | | | | | | | | | | | | | | | | |  
 Db 228 CCTACATTGTGAAGAACAAGCCTGTGGAGCTTCGCTGCCGCGCCTTCCCCGCCACACAGA 287

Qy 263 TCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCA 322  
 ||| | | | | | | | | | | | | | | | | | | | | |  
 Db 288 TCTACTTCAAGTGCAACGGCGAGTGGGTGAGCCAGAACGACCACGTACACAGGAAGGCC 347

Qy 323 CAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGG 382  
 || | | | | | | | | | | | | | | | | | | | | | |  
 Db 348 TGGATGAGGCCACCGGCCTGCGGGTGC GCGAGGTGCAGATCGAGGTGTCGCGGCAGCAGG 407

Qy 383 TCGAGAAGGTGTTGCGGGCTGGAGGAATACTGGTGCCAGTGCCTGGGCATGGAGCTCCTCGG 442  
 | ||| || | | | | | | | | | | | | | | | | | | |  
 Db 408 TGGAGGAGCTCTTTGGGCTGGAGGATTACTGGTGCCAGTGCCTGGCCTGGAGCTCCGCAG 467

Qy 443 GCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGC 502  
 ||||| | | | | | | | | | | | | | | | | | | | |  
 Db 468 GCACCACCAAGAGTCGCCGAGCCTACGTCCGCATCGCCTACCTGCGCAAGAACTTCGATC 527

Qy 503 AGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCAC 562  
 ||||| | | | | | | | | | | | | | | | | | | | |  
 Db 528 AGGAGCCTCTGGGCAAGGAGGTGCCCTGGACCATGAGGTTCTCCTGCAGTGCCGCCCGC 587

Qy 563 CGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGT 622  
 ||||| | | | | | | | | | | | | | | | | | | | |  
 Db 588 CGGAGGGGGTGCCTGTGGCCGAGGTGGAATGGCTCAAGAATGAGGATGTCATCGACCCCA 647

Qy 623 CCCTGGACCCCAATGTATACATCACGCGGGAGCACAGCCTGGTGGTGC GACAGGCCCGCC 682  
 ||| |||| |||| | | | | | | | | | | | | | | | |  
 Db 648 CCCAGGACACCAACTTCCTGCTCACCATCGACCACAACCTCATCATCCGCCAGGCCCGCC 707

Qy 683 TTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAACATCGTGGCACGTGCGCGCAGCG 742  
 | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 708 TGTGCGGACACTGCCAACTATACCTGCGTGGCCAAGAACATCGTGGCCAACGCCGGAGCA 767

Qy 743 CCTCCGCTGCTGTATCGTCTACGTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCG 802  
 || | || | | | | | | | | | | | | | | | | | | |  
 Db 768 CCACTGCCACCGTTCATCGTCTACGTGAATGGCGGCTGGTCCAGCTGGGCAGAGTGGTCAC 827

Qy 803 TCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGG 862  
 |||| | | | | | | | | | | | | | | | | | | | |  
 Db 828 CCTGCTCCAACCGCTGTGGCCGAGGCTGGCAGAAGCGCACCCGGACCTGCACCAACCCCG 887

Qy 863 CGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCA 922  
 | || | | | | | | | | | | | | | | | | | | | | |  
 Db 888 CTCCACTCAACGGAGGGGCTTCTGCGAGGGCCAGGCATTCCAGAAGACCGCCTGCACCA 947

Qy 923 CCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTTCGGCCTGTGGGCTGG 982  
 || | | | | | | | | | | | | | | | | | | | | | |  
 Db 948 CCATCTGCCCAGTCGATGGGGCGTGACGGAGTGGAGCAAGTGGTCAGCCTGCAGCACTG 1007

Qy 983 ACTGCACCCACTGGCGGAGCCGTGAGTGTCTGACCCAGCACCCCCGCAACGGAGGGGAGG 1042  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1008 AGTGTGCCCACTGGCGTAGCCGCGAGTGCATGGCGCCCCACCCCAGAACGGAGGCCGTG 1067

Qy 1043 AGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTG 1102  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1068 ACTGCAGCGGGACGCTGCTCGACTCTAAGAACTGCACAGATGGGCTGTGCATGCAACTGG 1127

Qy 1103 CTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGG 1162  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1128 AGGCCTCAGGGGATGCGGCGCTGTATGCGGGGCTCGTGGTGGCCATCTTCGTGGTCGTGG 1187

Qy 1163 TCCTGCTGCTGCTTGTCTCTCATCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAG 1222  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1188 CAATCCTCATGGCGGTGGGGGTGGTGGTGTACCGCCGCAACTGCCGTGACTTCGACACAG 1247

Qy 1223 ATGTGGCTGACTCGTCCATT---CTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCA 1279  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1248 ACATCACTGACTCATCTGCTGCCCTGACTGGTGGTTTCCACCCCGTCAACTTTAAGACGG 1307

Qy 1280 GCAAAGCAGACAACCCCCATCTGCT-----CACCATCCAGCCGGACCTCAGCACCACCA 1333  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1308 CAAGGCCAGTAACCCGCAGCTCCTACACCCCTCTGTGCCTCCTGACCTGACAGCCAGCG 1367

Qy 1334 CCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGA----- 1370  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1368 CCGGCATCTACCGCGGACCCGTGTATGCCCTGCAGGACTCCACCGACAAAATCCCCATGA 1427

Qy 1371 -----TGGGCCCAGCCCCAAGTTCCAGCTCACCA----- 1399  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1428 CCAACTCTCCTCTGCTGGACCCCTTACCCAGCCTTAAGGTCAAGGTCTACAGCTCCAGCA 1487

Qy 1400 --ATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACAC-----ACTGCACC 1447  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1488 CCACGGGCTCTGGGCCAGGCCTGGCAGATGGGGCTGACCTGCTGGGGGTCTTGCCGCCTG 1547

Qy 1448 ACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAGAATACT 1507  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1548 GCACATAACCTAGCGATTTCGCCCGGACACCCACTTCCTGCACCTGCGCAGCGCCAGCC 1607

Qy 1508 TCCGCTC-----CCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCT 1552  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1608 TCGGTTCCCAGCAGCTCTTGGGCCTGCCCCGAGACCCAGGGAGCAGCGTCAGCGGCACCT 1667

Qy 1553 TCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCC 1612  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1668 TTGGCTGCCTGGGTGGGAGGCTCAGCATCCCCGGCACAGGGGTGAGCTTGCTGGTGCCCA 1727

Qy 1613 CAGATGCCATACCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAG 1672  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1728 ATGGAGCCATTCCCCAGGGCAAGTTCTACGAGATGTATCTACTCATCAACAAGGCAGAAA 1787

Qy 1673 ACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGAC 1732  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1788 GTACCCTGCCGCTTTCAGAAGGGACCCAGACAGTATTGAGCCCCTCGGTGACCTGTGGAC 1847

Qy 1733 CCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCA 1792

Db	1848	CCACAGGCCTCCTGCTGTGCCGCCCCGTCATCCTCACCATGCCCCACTGTGCCGAAGTCA	1907
Qy	1793	GCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATG	1852
Db	1908	GTGCCCGTGACTGGATCTTTCAGCTCAAGACCCAGGCCACCAGGGCCACTGGGAGGAGG	1967
Qy	1853	TGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTG	1912
Db	1968	TGGTGACCCTGGATGAGGAGACCCTGAACACACCCTGCTACTGCCAGCTGGAGCCCAGGG	2027
Qy	1913	CCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCG	1972
Db	2028	CCTGTACATCCTGCTGGACCAGCTGGGCACCTACGTGTTACGGGCGAGTCCTATTCCC	2087
Qy	1973	TGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCG	2032
Db	2088	GCTCAGCAGTCAAGCGGCTCCAGCTGGCCGTCTTCGCCCCCGCCCTCTGCACCTCCCTGG	2147
Qy	2033	AGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGC	2092
Db	2148	AGTACAGCCTCCGGGTCTACTGCCTGGAGGACACGCCTGTAGCACTGAAGGAGGTGCTGG	2207
Qy	2093	AGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGG	2152
Db	2208	AGCTGGAGCGGACTCTGGGCGGATACTTGGTGGAGGAGCCGAAACCGCTAATGTTCAAGG	2267
Qy	2153	ACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTA	2212
Db	2268	ACAGTTACCACAACCTGCGCCTCTCCCTCCATGACCTCCCCATGCCCATTTGGAGGAGCA	2327
Qy	2213	AGCTCCTTGTCAGCTACCAGGAGATCCCCCTTTTATCACATCTGGAATGGCACGCAGCGGT	2272
Db	2328	AGCTGCTGGCCAAATACCAGGAGATCCCCTTCTATCACATTTGGAGTGGCAGCCAGAAGG	2387
Qy	2273	ACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCA	2332
Db	2388	CCCTCCACTGCACTTTCACCCTGGAGAGGCACAGCTTGGCCTCCACAGAGCTCACCTGCA	2447
Qy	2333	AGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCA	2392
Db	2448	AGATCTGCGTGCGGCAAGTGGAAGGGGAGGGCCAGATATTCCAGCTGCATACCACTCTGG	2507
Qy	2393	CCAAG---GACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAG	2449
Db	2508	CAGAGACACCTGCTGGCTCCCTGGACACTCTCTGCTCTGCCCTGGCAGCACTGTCACCA	2567
Qy	2450	CCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCA	2509
Db	2568	CCCAGCTGGGACCTTATGCCTTCAAGATCCCCTGTCCATCCGCCAGAAGATATGCAACA	2627
Qy	2510	GCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACC	2569
Db	2628	GCCTAGATGCCCCCAACTCACGGGGCAATGACTGGCGGATGTTAGCACAGAAGCTCTCTA	2687
Qy	2570	TGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACC	2629



XX  
PF 07-JAN-2002; 2002WO-US000375.  
XX  
PR 05-JAN-2001; 2001US-0260018P.  
PR 08-JAN-2001; 2001US-0260360P.  
PR 28-FEB-2001; 2001US-0272411P.  
PR 02-MAR-2001; 2001US-0272817P.  
PR 05-JUL-2001; 2001US-0303231P.  
PR 12-JUL-2001; 2001US-0305060P.  
PR 10-SEP-2001; 2001US-0318405P.  
PR 12-SEP-2001; 2001US-0318700P.  
PR 04-JAN-2002; 2002US-00037417.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Kekuda R, Alsobrook JP, Tchernev VT, Liu X, Spytek KA;  
PI Patturajan M, Grosse WM, Lepley DM, Burgess CE, Vernet CAM, Li L;  
PI Gorman L, Edinger S, Sciore P, Ellerman K, Malyankar U;  
PI Rothenberg M, Stone D, Boldog F, Guo X, Shenoy S, Anderson D;  
PI Padigar M, Taupier RJ, Miller CE, Eisen A;  
XX  
DR WPI; 2002-583619/62.  
DR P-PSDB; ABB09520.  
XX  
PT Novel polypeptides and nucleic acids homologous to transmembrane  
PT receptor, thymosin, neuromodulin-like family of proteins for diagnosing,  
PT treating cancer, atherosclerosis, neurological, skin and autoimmune  
PT disorders.  
XX  
PS Claim 9a; Page 121; 323pp; English.  
XX  
CC The invention relates to 24 novel human proteins designated NOV1-NOV14  
CC (ABB09501-ABB09524), collectively referred to as NOVX proteins, and  
CC nucleic acids encoding them (ABQ93879-ABQ93902). NOVX proteins and  
CC nucleotides are useful in the treatment, diagnosis or prevention of NOVX-  
CC associated disorders or in the manufacture of a medicament for treating  
CC such disorders, with specific applications described for each of the 24  
CC NOVX proteins, based on their homology to known proteins. Various  
CC disorders are associated with NOVX proteins including neurological  
CC disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases),  
CC pain, behavioural disorders, addiction, tuberous sclerosis, cancers  
CC (e.g., colorectal cancer, leukaemia and osteosarcoma), immune disorders  
CC (e.g., allergies and autoimmune diseases), myasthenia gravis, asthma,  
CC various forms of arthritis, diabetes, thyroiditis, cardiovascular disease  
CC (e.g., hypertension), reproductive disorders, endometriosis,  
CC incontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis,  
CC cirrhosis, glomerular endotheliosis, polycystic kidney disease, endocrine  
CC disorders, obesity, bacterial infections and particularly cardiomyopathy,  
CC atherosclerosis, cell signal processing-related disorders and disorders  
CC of metabolic pathway regulation. NOVX nucleic acids and polypeptides may  
CC be used to identify cellular receptors or downstream effectors which  
CC binds to a NOVX protein, and are also useful as targets for the  
CC identification of small molecules that modulate or inhibit processes such  
CC as neurogenesis, cell differentiation, cell motility, cellular  
CC proliferation, haematopoiesis, wound healing and angiogenesis. NOVX  
CC nucleic acid sequences can be used to identify a cell or tissue type and  
CC are useful as a source of primers or probes for forensic biology and for

CC identifying and cloning NOVX homologues in other cell types. Cells  
CC comprising NOVX nucleic acids are useful for producing non-human  
CC transgenic animals which are useful for studying the function and  
CC activity of NOVX proteins and for identifying and evaluating modulators  
CC of NOVX activity. The present sequence represents DNA encoding the  
CC transmembrane receptor UNC5H2-like protein NOV11. The gene encoding NOV11  
CC is located on chromosome 10

XX

SQ Sequence 2895 BP; 557 A; 960 C; 854 G; 524 T; 0 U; 0 Other;

Query Match 33.2%; Score 913.6; DB 6; Length 2895;  
Best Local Similarity 61.6%; Pred. No. 5.1e-167;  
Matches 1684; Conservative 0; Mismatches 919; Indels 129; Gaps 9;

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Qy      143 ACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATG 202
          || | | | ||      ||      | || | ||| ||| ||||| ||| ||| |
Db      140 ACTCCTTCCCGTCAGCGCCAGCAGAGCCGCTGCCCTACTTCCTGCAGGAGCCACAGGACG 199

Qy      203 TGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGA 262
          ||||| || ||||| ||||| ||| ||| ||| ||| ||||| |||||
Db      200 CCTACATTGTGAAGAACAAGCCTGTGGAGCTCCGCTGCCGCGCCTTCCCCGCCACACAGA 259

Qy      263 TCTTCTTCAAGTGCAACGGGGAGTGGGTGCCCGAGGTGGACCACGTGATCGAGCGCAGCA 322
          ||| ||||| ||||| ||||| ||||| ||||| ||| ||| ||
Db      260 TCTACTTCAAGTGCAACGGCGAGTGGGTGAGCCAGAACGACCACGTACACAGGAAGGCC 319

Qy      323 CAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGG 382
          || | | | || || ||||      |||| | || | || | |||||
Db      320 TGGATGAGGCCACCGGTCTGCGGGTGCGCGAGGTGCAGATCGAGGTGTCGCGGCAGCAGG 379

Qy      383 TCGAGAAGGTGTTTCGGGCTGGAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGG 442
          | ||| || | || ||||| ||||| ||||| ||||| ||||| |||
Db      380 TGGAGGAGCTCTTTGGGCTGGAGGATTACTGGTGCCAGTGCGTGGCCTGGAGCTCCGCGG 439

Qy      443 GCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGC 502
          ||||| ||||| ||||| ||||| ||| | ||||| ||||| |||
Db      440 GCACCACCAAGAGTCGCCGAGCCTACGTCCGCATCGCCTGTCTGCGCAAGAACTTCGATC 499

Qy      503 AGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCAC 562
          ||||| |||| ||||| ||||| ||||| || | | ||| |||| |||
Db      500 AGGAGCCTCTGGGCAAGGAGGTGCCCCCTGGACCATGAGGTTCTCCTGCAGTGCCGCCCCG 559

Qy      563 CGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGT 622
          ||||| || ||| ||||| ||||| ||||| ||| |||| | | ||||
Db      560 CGGAGGGGGTGCCTGTGGCCGAGGTGGAATGGCTCAAGAATGAGGATGTCATCGACCCCA 619

Qy      623 CCCTGGACCCCAATGTATACATCACGCGGGAGCACAGCCTGGTGGTGCACAGGCCCGCC 682
          ||| |||| |||| | |||| || |||| ||| | | |||||
Db      620 CCCAGGACACCAACTTCCTGCTCACCATCGACCACAACCTCATCATCCGCCAGGCCCGCC 679

Qy      683 TTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAACATCGTGGCACGTGCGCGCAGCG 742
          | | |||| ||||| ||||| ||||| ||||| ||||| ||| |||
Db      680 TGTGCGGACACTGCCAACTATACCTGCGTGGCCAAGAACATCGTGGCCAACGCCGGAGCA 739

Qy      743 CCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCG 802
          || | || | ||||| ||||| || || |||| | ||| | |||||
Db      740 CCACTGCCACCGTCATCGTCTACGTGAATGGCGGCTGGTCCAGCTGGGCAGAGTGGTCAC 799
```

Qy 803 TCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGG 862  
 ||| | | ||||| || ||||| ||| | |||| | ||||| ||| |  
 Db 800 CCTGCTCCAACCGCTGTGGCCGAGGCTGGCAGAAGCGCACCCGGACCTGCACCAACCCCG 859

Qy 863 CGCCTCTCAACGGGGGCGCTTCTGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCA 922  
 | | ||||| | | |||| | |||| | |||| | |||| | |||  
 Db 860 CTCCACTCAACGGAGGGGCC'TCTGCGAGGGCCAGGCATTCCAGAAGACCGCCTGCACCA 919

Qy 923 CCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGG 982  
 || | ||||| || || |||| | ||||| ||||| |||| | | |  
 Db 920 CCATCTGCCCAGTCGATGGGGCGTGGACGGAGTGGAGCAAGTGGTCAGCCTGCAGCACTG 979

Qy 983 ACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGG 1042  
 | | ||||| |||| | |||| | | |||| | |||| | |  
 Db 980 AGTGTGCCCACTGGCGTAGCCGCGAGTGCATGGCGCCCCACCCAGAACGGAGGCCGTG 1039

Qy 1043 AGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTG 1102  
 | || | || | |||| | |||| | || | || | || |||  
 Db 1040 ACTGCAGCGGGACGCTGCTCGACTCTAAGAACTGCACAGATGGGCTGTGCATGCAAAGTG 1099

Qy 1103 CTT-----TGGCCCTGAGGACGTGGCCCTCT 1129  
 || | | | || | || | ||  
 Db 1100 AGTCACAGTGTGGTCCTCCTGTCCCCGCGAGTGTGGAGGCCTCAGGGGATGCGGCGCTGT 1159

Qy 1130 ATGTGGGCCTC---ATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCATCC 1186  
 ||| ||| || | ||| | ||| | || | || | || |  
 Db 1160 ATGCGGGGCTCGTGGTGGCCATCTTCGTGGTGTGGCAATCCTCATGGCGGTGGGGGTGG 1219

Qy 1187 TCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATT---C 1243  
 | || | |||| | | | |||| | | |||| | || |  
 Db 1220 TGGTGTACCGCCGCAACTGCCGTGACTTCGACACAGACATCACTGACTCATCTGCTGCCC 1279

Qy 1244 TCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGC 1303  
 | || | |||| | |||| | |||| | | | |||| | || |  
 Db 1280 TGA CTGGTGGTTTCCACCCCGTCAACTTTAAGACGGCAAGGCCAGTAACCCGCAGCTCC 1339

Qy 1304 T-----CACCATCCAGCCGGACCTCAGCACCACCACCACCCTACCAGGGCAGTCTCT 1357  
 | | | | |||| | ||| | | |||| | || |  
 Db 1340 TACACCCCTCTGTGCCTCCTGACCTGACAGCCAGCGCCGGCATCTACCGCGGACCCGTGT 1399

Qy 1358 GTCCCCGGCAGGA-----TG 1372  
 | ||| |||||  
 Db 1400 ATGCCCTGCAGGACTCCACCGACAAAATCCCCATGACCAACTCTCCTCTGCTGGACCCCT 1459

Qy 1373 GGCCAGCCCCAAGTTCCAGCTCACCA-----ATGGGCACCTGCTCAGCCCCCT 1421  
 ||||| ||| || || || || | |||| | | ||| ||  
 Db 1460 TACCCAGCCTTAAGGTCAAGGTCTACAGCTCCAGCACCACGGGCTCTGGGCCAGGCCTGG 1519

Qy 1422 GGGTGGCGGCCGCCACAC-----ACTGCACCACAGCTCTCCACCTCTGAGGCCG 1471  
 | | ||| | | | || | || | || | | |||  
 Db 1520 CAGATGGGGCTGACCTGCTGGGGGTCTTGCCGCCTGGCACATAACCTAGCGATTTCGCCC 1579

Qy 1472 AGGAGTTCGTCTCCCGCCTCTCCACCCAGAACTACTTCCGCTC-----CC 1516  
 ||| | ||| | | | | ||| | ||| ||  
 Db 1580 GGGACACCCACTTCTGACCTGCGCAGCGCCAGCCTCGGTTCACGAGCTCTTGGGCC 1639

Qy 1517 TGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGA 1576  
 ||||| | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1640 TGCCCCGAGACCCAGGGAGCAGCGTCAGCGGCACCTTTGGCTGCCTGGGTGGGAGGCTCA 1699

Qy 1577 TGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCCATAACCCGAGGGAAGA 1636  
 |||| | |||| | || | | | | | | | | | | | | | | | | |  
 Db 1700 GCATCCCCGGCACAGGTGTCAGCTTGTGGTGCCCAATGGAGCCATTCCCCAGGGCAAGT 1759

Qy 1637 TCTATGAGATCTACCTCAGCTGCACAAGCCGGAAGACGTGAGGTTGCCCCTAGCTGGCT 1696  
 ||| |||| | | | | | | | | | | | | | | | | | | | | | |  
 Db 1760 TCTACGAGATGTATCTACTCATCAACAAGGCAGAAAGTACCCTGCCGCTTTCAGAAGGGA 1819

Qy 1697 GTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCTGGCGTCCTGCTCACCCGGC 1756  
 |||| | | ||| || | | | | | | | | | | | | | | | | | |  
 Db 1820 CCCAGACAGTATTGAGCCCCCTCGGTGACCTGTGGACCCACAGGCCTCCTGCTGTGCCGCC 1879

Qy 1757 CAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGACAGCTGGAGCCTGCGCC 1816  
 | ||||| | | | | | | | | | | | | | | | | | | | | | |  
 Db 1880 CCGTCATCCTCACCATGCCCCACTGTGCCGAAGTCAGTGCCCGTGACTGGATCTTTCAGC 1939

Qy 1817 TCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGC 1876  
 |||| | ||| | | |||| | ||||| || | | |||| | |||| | | |  
 Db 1940 TCAAGACCCAGGCCACCAGGGCCACTGGGAGGAGGTGGTGACCCTGGATGAGGAGACCC 1999

Qy 1877 CCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGC 1936  
 | | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 2000 TGAACACACCCTGCTACTGCCAGCTGGAGCCCAGGGCCTGTCACATCCTGCTGGACCAGC 2059

Qy 1937 TGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGC 1996  
 |||| | | | | | ||| || | | | | | | | | | | | | | | |  
 Db 2060 TGGGCACCTACGTGTTACAGGGCGAGTCTATTCCCGCTCAGCAGTCAAGCGGCTCCAGC 2119

Qy 1997 TGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCC 2056  
 || | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 2120 TGGCCGTCTTCGCCCCGCCCTCTGCACCTCCCTGGAGTACAGCCTCCGGGTCTACTGCC 2179

Qy 2057 TGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGAC 2116  
 || | |||| | | |||| | ||||| || | ||||| | | |||| | | |  
 Db 2180 TGGAGGACACGCCTGTAGCACTGAAGGAGGTGCTGGAGCTGGAGCGGACTCTGGCGGAT 2239

Qy 2117 AGCTGATCCAGGAGCCACGGGTCTGCACCTCAAGGACAGTTACCACAACCTGCGCCTAT 2176  
 | || | |||| | | | | | | | | | | | | | | | | | | | | |  
 Db 2240 ACTTGGTGGAGGAGCCGAAACCGCTAATGTTCAAGGACAGTTACCACAACCTGCGCCTCT 2299

Qy 2177 CCATCCACGATGTGCCAGCTCCCTGTGGAAGAGTAAGCTCCTTGTGAGCTACCAGGAGA 2236  
 || |||| | | || | || | || | || | || | || | || | || | || |  
 Db 2300 CCCTCCATGACCTCCCCATGCCATTGGAGGAGCAAGCTGCTGGCCAAATACCAGGAGA 2359

Qy 2237 TCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCACTGCACCTTCACCCTGG 2296  
 ||||| ||||| |||| | || | || | || | || | || | || | || |  
 Db 2360 TCCCCTTCTATCACATTTGGAGTGGCAGCCAGAAGGCCCTCCACTGCACTTTCACCCTGG 2419

Qy 2297 AGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGG 2356  
 || | |||| | | | || | || | || | || | || | || | || | || |  
 Db 2420 AGAGGCACAGCTTGGCCTCCACAGAGCTCACCTGCAAGATCTGCGTGCGGCAAGTGGAAAG 2479

Qy 2357 GCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAG---GACACAAGGTTTGCTG 2413



Db	2480	GGGAGGGCCAGATATTCCAGCTGCATACCACTCTGGCAGAGACACCTGCTGGCTCCCTGG	2539
Qy	2414	AGCTGCTGGCTCTGGAGAGTGAAGCGGGGTCCCAGCCCTGGTGGGCCCCAGTGCCTTCA	2473
Db	2540	ACACTCTCTGCTCTGCCCCCTGGCAGCACTGTCACCACCCAGCTGGGACCTTATGCCTTCA	2599
Qy	2474	AGATCCCCCTTCCTCATTTCGGCAGAAGATAATTTCCAGCCTGGACCCACCTGTAGGCGGG	2533
Db	2600	AGATCCCCACTGTCCATCCGCCAGAAGATATGCAACAGCCTAGATGCCCCAACTCACGGG	2659
Qy	2534	GTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAGCCATCTCAGCTTCTTTG	2593
Db	2660	GCAATGACTGGCGGATGTTAGCACAGAAGCTCTCTATGGACCGGTACCTGAATTACTTTG	2719
Qy	2594	CCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCGCGGCACTTCCCCA	2653
Db	2720	CCACCAAAGCGAGCCCCACGGGTGTGATCCTGGACCTCTGGGAAGCTCTGCAGCAGGACG	2779
Qy	2654	ACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAGCCAGACGCTGGCC	2713
Db	2780	ATGGGGACCTCAACAGCCTGGCGAGTGCCTTGGAGGAGATGGGCAAGAGTGAGATGCTGG	2839
Qy	2714	TCTTCACAGTGTTCGGAGGCTGAGTGCTGAGGC	2745
Db	2840	TGGCTGTGGCCACCGACGGGGACTGCTGAGCC	2871

RESULT 15

AAS21316

ID AAS21316 standard; cDNA; 3884 BP.

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AC AAS21316;

XX

DT 24-OCT-2001 (first entry)

XX

DE Human cDNA sequence encoding for PRO4326 polypeptide.

XX

KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;  
 KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;  
 KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;  
 KW A-peptide; factor VIIA; gene therapy; ss.

XX

OS Homo sapiens.

XX

PN WO200140466-A2.

XX

PD 07-JUN-2001.

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PF 01-DEC-2000; 2000WO-US032678.

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PR 01-DEC-1999; 99WO-US028301.

PR 01-DEC-1999; 99WO-US028634.

PR 02-DEC-1999; 99WO-US028551.

PR 02-DEC-1999; 99WO-US028564.

PR 02-DEC-1999; 99WO-US028565.

PR 09-DEC-1999; 99US-0170262P.

PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 03-MAR-2000; 2000US-0187202P.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 05-JUN-2000; 2000US-0209832P.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.

XX

PA (GETH ) GENENTECH INC.

XX

PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX

DR WPI; 2001-408281/43.

DR P-PSDB; AAU12244.

XX

PT Isolated , secretory and transmembrane PRO polypeptide used to detect  
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO  
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,  
PT breast, prostate, cervical.

XX

PS Claim 3; Fig 145; 813pp; English.

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CC AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO  
CC polypeptides. The PRO polypeptides are useful to detect other PRO  
CC polypeptides, to link bioactive molecules to cells expressing PRO  
CC polypeptides, to modulate biological activities of cells expressing PRO  
CC polypeptides, and to detect the presence of mammalian lung, colon,  
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
CC polypeptide expression in a cell sample to that in a control sample. Some

CC of the 275 sequences are also useful to stimulate the release of tumour  
 CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or  
 CC differentiation of chondrocytes, the proliferation or gene expression in  
 CC pericyte cells, the release of proteoglycans from cartilage, the  
 CC proliferation of inner ear utricular supporting cells or of T-  
 CC lymphocytes, the release of a cytokine from peripheral blood monocytes  
 CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO  
 CC polypeptides may modulate glucose or free fatty acid uptake by skeletal  
 CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor  
 CC VIIA. The PRO polypeptides can be used in assays to identify molecules  
 CC involved in binding interactions. The polynucleotides encoding PRO  
 CC polypeptides can be used to generate probes, antisense RNA/DNA,  
 CC transgenic or knock out animals and can be used in gene therapy

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SQ Sequence 3884 BP; 767 A; 1278 C; 1162 G; 677 T; 0 U; 0 Other;

Query Match 32.8%; Score 902.4; DB 4; Length 3884;  
 Best Local Similarity 61.4%; Pred. No. 7.7e-165;  
 Matches 1677; Conservative 0; Mismatches 926; Indels 129; Gaps 9;

Qy	143	ACCCAGTGCCTGGTGCCAAACCCGACCTGCTTCCCCACTTCTGGTGGAGCCCGAGGATG	202
Db	507	ACTCCTTCCCGTCAGCGCCAGCAGAGCCGCTGCCCTACTTCTGCAGGAGCCACAGGACG	566
Qy	203	TGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGA	262
Db	567	CCTACATTGTGAAGAACAAGCCTGTGGAGTCCGCTGCCGCGCCTTCCCCGCCACACAGA	626
Qy	263	TCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCA	322
Db	627	TCTACTTCAAGTGCAACGGCGAGTGGGTGAGCCAGAACGACCACGTACACAGGAAGGCC	686
Qy	323	CAGACGGGAGCAGTGGGCTGCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGG	382
Db	687	TGGATGAGGCCACCGGCCTGCGGGTGCGGAGGTGCAGATCGAGGTGTCGCGGCAGCAGG	746
Qy	383	TCGAGAAGGTGTTTCGGGCTGGAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGG	442
Db	747	TGGAGGAGCTCTTTGGGCTGGAGGATTACTGGTGCCAGTGCGTGGCCTGGAGCTCCGCAG	806
Qy	443	GCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGC	502
Db	807	GCACCACCAAGAGTCGCCGAGCCTACGTCCGCATCGCCTACCTGCGCAAGAACTTCGATC	866
Qy	503	AGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCAC	562
Db	867	AGGAGCCTCTGGGCAAGGAGGTGCCCTGGACCATGAGGTTCTCCTGCAGTGCCGCCCGC	926
Qy	563	CGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGT	622
Db	927	CGGAGGGGTGCTGTGGCCGAGGTGGAATGGCTCAAGAATGAGGATGTCATCGACCCCA	986
Qy	623	CCCTGGACCCCAATGTATACATCACGCGGAGCACAGCCTGGTGGTGCACAGGCCCGCC	682
Db	987	CCCAGGACACCAACTTCCTGCTCACCATCGACCACAACCTCATCATCCGCCAGGCCCGCC	1046
Qy	683	TTGCTGACACGGCCAACCTACACCTGCGTGGCCAAGAACATCGTGGCACGTGCGCGCAGCG	742

Db	1047	TGTCGGACACTGCCAACTATACCTGCGTGGCCAAGAACATCGTGGCCAAACGCCGGAGCA	1106
Qy	743	CCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCG	802
Db	1107	CCACTGCCACCGTCATCGTCTACGTGAATGGCGGCTGGTCCAGCTGGGCAGAGTGGTCAC	1166
Qy	803	TCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGG	862
Db	1167	CCTGCTCCAACCGCTGTGGCCGAGGCTGGCAGAAGCGCACCCGGACCTGCACCAACCCCG	1226
Qy	863	CGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCA	922
Db	1227	CTCCACTCAACGGAGGGGCCCTTCTGCGAGGGCCAGGCATTCCAGAAGACCGCCTGCACCA	1286
Qy	923	CCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGG	982
Db	1287	CCATCTGCCCAGTCGATGGGGCGTGGACGGAGTGGAGCAAGTGGTCAGCCTGCAGCACTG	1346
Qy	983	ACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGG	1042
Db	1347	AGTGTGCCCACTGGCGTAGCCGCGAGTGCATGGCGCCCCACCCAGAACGGAGGCCGTG	1406
Qy	1043	AGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGT-	1101
Db	1407	ACTGCAGCGGGACGCTGCTCGACTCTAAGAACTGCACAGATGGGCTGTGCATGCAAAATA	1466
Qy	1102	-----GCTTCTGGCCCTGAGGACGTGGCCCTCT	1129
Db	1467	AGAAAACCTCTAAGCGACCCCAACAGCCACCTGCTGGAGGCCTCAGGGGATGCGGCGCTGT	1526
Qy	1130	ATGTGGGCCTC---ATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCATCC	1186
Db	1527	ATGCGGGGCTCGTGGTGGCCATCTTCGTGGTCTGGCAATCCTCATGGCGGTGGGGGTGG	1586
Qy	1187	TCGTTTATTGCCGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATT---C	1243
Db	1587	TGGTGTACCGCCGCAACTGCCGTGACTTCGACACAGACATCACTGACTCATCTGCTGCC	1646
Qy	1244	TCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGC	1303
Db	1647	TGACTGGTGGTTTCCACCCCGTCAACTTTAAGACGGCAAGGCCAGCAACCCGCAGCTCC	1706
Qy	1304	T-----CACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCT	1357
Db	1707	TACACCCCTCTGTGCCTCCTGACCTGACAGCCAGCGCCGGCATCTACCGCGGACCCGTGT	1766
Qy	1358	GTCCCCGGCAGGA-----TG	1372
Db	1767	ATGCCCTGCAGGACTCCACCGACAAAATCCCCATGACCAACTCTCCTCTGCTGGACCCCT	1826
Qy	1373	GGCCCAGCCCCAAGTTCCAGCTCACCA-----ATGGGCACCTGCTCAGCCCCCT	1421
Db	1827	TACCCAGCCTTAAGGTCAAGGTCTACAGCTCCAGCACCACGGGCTCTGGGCCAGGCCTGG	1886
Qy	1422	GGGTGGCGGGCCGCACAC-----ACTGCACCACAGCTCTCCACCTCTGAGGCCG	1471

Db 1887 CAGATGGGGCTGACCTGCTGGGGGTCTTGCCGCCTGGCACATACCCTAGCGATTTCGCCC 1946

Qy 1472 AGGAGTTCGTCTCCCGCCTCTCCACCCAGAACTACTTCCGCTC-----CC 1516  
 ||| | ||| | | | | | | | | | | ||

Db 1947 GGGACACCCACTTCCTGCACCTGCGCAGCGCCAGCCTCGGTTCCAGCAGCTCTTGGGGC 2006

Qy 1517 TGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGA 1576  
 ||||| ||| | | | | | | | | | | | | | |

Db 2007 TGCCCCGAGACCCAGGGAGCAGCGTCAGCGGCACCTTTGGCTGCCTGGGTGGGAGGCTCA 2066

Qy 1577 TGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCCATACCCCGAGGGAAGA 1636  
 |||| | |||| | |||| | | | | | | | | | | | |

Db 2067 GCATCCCCGGCACAGGGGTGAGCTTGCTGGTGCCCAATGGAGCCATTCCCCAGGGCAAGT 2126

Qy 1637 TCTATGAGATCTACCTCAGCTGCACAAGCCGGAAGACGTGAGGTTGCCCTAGCTGGCT 1696  
 |||| |||| | | | | | | | | | | | | | |

Db 2127 TCTACGAGATGTATCTACTCATCAACAAGGCAGAAAGTACCCTCCCGCTTTCAGAAGGGA 2186

Qy 1697 GTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCTGGCGTCCTGCTCACCCGGC 1756  
 |||| | |||| || | | | | | | | | | | | | |

Db 2187 CCCAGACAGTATTGAGCCCTCGGTGACCTGTGGACCCACAGGCCTCCTGCTGTGCCGCC 2246

Qy 1757 CAGTCATCCTGGCTATGGACCACTGTGGGGAGCCAGCCCTGACAGCTGGAGCCTGCGCC 1816  
 | ||||| || | || | ||||| || | || | |||| | | | |

Db 2247 CCGTCATCCTCACCATGCCCCACTGTGCCAAGTCAGTGCCCGTGACTGGATCTTTCAGC 2306

Qy 1817 TCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGC 1876  
 |||| | || | | | |||| | ||||| || | || | |||| | ||

Db 2307 TCAAGACCCAGGCCACCAGGGCCACTGGGAGGAGGTGGTGACCCTGGATGAGGAGACCC 2366

Qy 1877 CCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCCTGCTACGTCTTCACCGAGCAGC 1936  
 | | | | ||||| ||||| |||| | | | | | | | |

Db 2367 TGAACACACCCTGCTACTGCCAGCTGGAGCCCAGGGCCTGTACATCCTGCTGGACCAGC 2426

Qy 1937 TGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGC 1996  
 |||| || | | || | || | | | | | | | | | | |

Db 2427 TGGGCACCTACGTGTTACGGGCGAGTCCTATTCCCGCTCAGCAGTCAAGCGGCTCCAGC 2486

Qy 1997 TGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCC 2056  
 || | || | || | | | ||||| ||||| ||||| ||||| |||||

Db 2487 TGGCCGTCTTCGCCCCCGCCCTCTGCACCTCCCTGGAGTACAGCCTCCGGGTCTACTGCC 2546

Qy 2057 TGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGAC 2116  
 || | |||| | | |||| | ||||| || | |||| | |||| |

Db 2547 TGGAGGACACGCCTGTAGCACTGAAGGAGGTGCTGGAGCTGGAGCGGACTCTGGGCGGAT 2606

Qy 2117 AGCTGATCCAGGAGCCACGGGTCTGCACTTCAAGGACAGTTACCACAACCTGCGCCTAT 2176  
 | || | |||| | | ||||| ||||| ||||| ||||| |||||

Db 2607 ACTTGGTGGAGGAGCCGAAACCGCTAATGTTCAAGGACAGTTACCACAACCTGCGCCTCT 2666

Qy 2177 CCATCCACGATGTGCCAGCTCCCTGTGGAAGAGTAAGCTCCTTGTCAGCTACCAGGAGA 2236  
 || |||| | | || | || | || | || | || | || | ||

Db 2667 CCCTCCATGACCTCCCCATGCCATTGGAGGAGCAAGCTGCTGGCCAAATACCAGGAGA 2726

Qy 2237 TCCCCTTTATCACATCTGGAATGGCAGCGAGCGGTACTTGCACTGCACCTTCACCCTGG 2296  
 ||||| ||||| |||| | || | || | || | || | || | ||

Db 2727 TCCCCTTCTATCACATTTGGAGTGGCAGCCAGAAGGCCCTCCACTGCACTTTCACCCTGG 2786

Qy 2297 AGCGTGTCAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGG 2356  
 || | ||| | | | ||| ||| ||| ||| ||| ||| |  
 Db 2787 AGAGGCACAGCTTGGCCTCCACAGAGCTCACCTGCAAGATCTGCGTGCGGCAAGTGGGAAG 2846

Qy 2357 GCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAG---GACACAAGGTTTGCTG 2413  
 | || || ||| || | | || | | || | | || |  
 Db 2847 GGGAGGGCCAGATATTCCAGCTGCATACCACTCTGGCAGAGACACCTGCTGGCTCCCTGG 2906

Qy 2414 AGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGCCCCAGTGCCTTCA 2473  
 | || | | || | || ||| | ||| | ||| ||| ||| |||  
 Db 2907 AACTCTCTGCTCTGCCCCCTGGCAGCACTGTCAACCACCCAGCTGGGACCTTATGCCTTCA 2966

Qy 2474 AGATCCCCCTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGACCCACCCTGTAGGCGGG 2533  
 ||||| | ||| || ||||| ||||| || | ||| ||||  
 Db 2967 AGATCCCCTGTCCATCCGCCAGAAGATATGCAACAGCCTAGATGCCCCAACTCACGGG 3026

Qy 2534 GTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAGCCATCTCAGCTTCTTTG 2593  
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 Db 3027 GCAATGACTGGCGGATGTTAGCACAGAAGCTCTCTATGGACCGGTACCTGAATTACTTTG 3086

Qy 2594 CCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCGCGGCACTTCCCCA 2653  
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 Db 3087 CCACCAAAGCGAGCCCCACGGGTGTGATCCTGGACCTCTGGGAAGCTCTGCAGCAGGACG 3146

Qy 2654 ACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAGCCAGACGCTGGCC 2713  
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 Db 3147 ATGGGGACCTCAACAGCCTGGCGAGTGCCTTGGAGGAGATGGGCAAGAGTGAGATGCTGG 3206

Qy 2714 TCTTCACAGTGTGCGAGGCTGAGTGCTGAGGC 2745  
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 Db 3207 TGGCTGTGGCCACCGACGGGGACTGCTGAGCC 3238

Search completed: July 7, 2004, 11:34:22  
 Job time : 1025 secs

OM nucleic - nucleic search, using sw model

Run on: July 7, 2004, 10:54:31 ; Search time 186 Seconds  
(without alignments)  
8210.886 Million cell updates/sec

Title: US-10-624-932-1  
Perfect score: 2752  
Sequence: 1 ccgcggggcccccgcgcccg.....tgagtgctgaggccggccag 2752

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
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	2	2259	82.1	3014	3	US-09-306-902A-1			Sequence 1, Appli
	3	1562.4	56.8	1787	2	US-08-808-982-2			Sequence 2, Appli
	4	1562.4	56.8	1787	3	US-09-306-902A-2			Sequence 2, Appli
	5	1155.8	42.0	1282	4	US-09-833-381-1806			Sequence 1806, Ap
	6	841.4	30.6	2831	2	US-08-808-982-3			Sequence 3, Appli
	7	841.4	30.6	2831	3	US-09-306-902A-3			Sequence 3, Appli
	8	432	15.7	1605	4	US-09-833-381-1807			Sequence 1807, Ap
	9	269	9.8	771	1	US-08-253-155A-17			Sequence 17, Appl
	10	119	4.3	305	2	US-08-808-982-4			Sequence 4, Appli
	11	119	4.3	305	3	US-09-306-902A-4			Sequence 4, Appli

12	53.6	1.9	657	3	US-08-985-526-2	Sequence 2, Appli
13	53.6	1.9	1326	3	US-08-985-526-4	Sequence 4, Appli
14	52.8	1.9	699	4	US-09-252-991A-7947	Sequence 7947, Ap
15	52.8	1.9	1302	4	US-09-252-991A-7809	Sequence 7809, Ap
c 16	52.8	1.9	1947	4	US-09-252-991A-7533	Sequence 7533, Ap
17	52.4	1.9	1770	4	US-09-252-991A-12265	Sequence 12265, A
18	52.4	1.9	4884	4	US-09-252-991A-12126	Sequence 12126, A
c 19	52.4	1.9	4884	4	US-09-252-991A-12292	Sequence 12292, A
20	52	1.9	7231	4	US-09-919-172-64	Sequence 64, Appl
21	50.8	1.8	3885	4	US-09-369-364A-16	Sequence 16, Appl
22	48.8	1.8	2493	4	US-09-252-991A-11987	Sequence 11987, A
c 23	48.8	1.8	2991	4	US-09-252-991A-12025	Sequence 12025, A
c 24	48.6	1.8	1068	4	US-09-252-991A-9933	Sequence 9933, Ap
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26	48.4	1.8	925	3	US-08-858-003-1	Sequence 1, Appli
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c 31	48	1.7	8312	4	US-09-620-312D-1048	Sequence 1048, Ap
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38	47	1.7	7218	1	US-08-232-463-14	Sequence 14, Appl
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42	45.2	1.6	987	4	US-09-252-991A-7285	Sequence 7285, Ap
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c 44	45.2	1.6	1575	4	US-09-252-991A-7330	Sequence 7330, Ap
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#### ALIGNMENTS

##### RESULT 1

US-08-808-982-1

; Sequence 1, Application US/08808982

; Patent No. 5939271

##### ; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; APPLICANT: Leonardo, E. David

; APPLICANT: Hink, Lindsay

; APPLICANT: Masu, Masayuki

; APPLICANT: Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 8

##### ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA



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;      ZIP: 94104
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/808,982
;      FILING DATE:
;      CLASSIFICATION: 530
;      ATTORNEY/AGENT INFORMATION:
;      NAME: OSMAN, RICHARD A
;      REGISTRATION NUMBER: 36,627
;      REFERENCE/DOCKET NUMBER: UC96-217
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (415) 343-4341
;      TELEFAX: (415) 343-4342
;      INFORMATION FOR SEQ ID NO: 1:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 3014 base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: double
;      TOPOLOGY: linear
;      MOLECULE TYPE: cDNA
US-08-808-982-1

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Query Match          82.1%; Score 2259; DB 2; Length 3014;
Best Local Similarity 89.7%; Pred. No. 0;
Matches 2427; Conservative 0; Mismatches 280; Indels 0; Gaps 0;

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Qy      46 ATGGCCGTC CGGCCCGGCCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTC 105
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Db     61 CGTGGTTTCGGGTGCCAGCAGAGTGCCACGGTGGCCAATCCAGTGCCCGGTGCCAACCCC 120

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Qy	766	GTGAACGGTGGGTGGTGCACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGC	825
Db	721	GTGAACGGTGGGTGGTGCACGTGGACTGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGT	780
Qy	826	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTC	885
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Db	841	TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACTCTGTGCCCAGTGGATGGGAGC	900
Qy	946	TGGAGCCCGTGGAGCAAGTGGTTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGT	1005
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Qy	1006	GAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGAC	1065
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Qy	1066	ACCCGCAACTGTACCAAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCC	1125
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Qy	1246	ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTC	1305
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Qy	1786	GAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG	1845
Db	1741	GAGCCCAGCCCTGACAGCTGGAGTCTGCGCCTCAAAAAGCAGTCCTGCGAGGGCAGTTGG	1800
Qy	1846	GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAG	1905
Db	1801	GAGGATGTGCTGCACCTTGGTGAGGAGTCACCTTCCACCTCTACTACTGCCAGCTGGAG	1860
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Db	1861	GCCGGGGCCTGCTATGTCTTCACGGAGCAGCTGGGCGGCTTTGCCCTGGTAGGAGAGGCC	1920
Qy	1966	CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC	2025
Db	1921	CTCAGCGTGGCTGCCACCAAGCGCCTCAGGCTCCTTCTGTTTGCTCCCGTGGCCTGTACG	1980
Qy	2026	TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG	2085
Db	1981	TCCCTTGAGTACAACATCCGAGTGTACTGCCTACACGACACCCACGACGCTCTCAAGGAG	2040
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RESULT 2
US-09-306-902A-1
; Sequence 1, Application US/09306902A
; Patent No. 6277585
;   GENERAL INFORMATION:
;       APPLICANT: Tessier-Lavigne, Marc
;               Leonardo, E. David
;               Hink, Lindsay
;               Masu, Masayuki
;               Kazuko, Keino-Masu
;   TITLE OF INVENTION: Netrin Receptors
;   NUMBER OF SEQUENCES: 9
;   CORRESPONDENCE ADDRESS:

```

```

;      ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;      STREET: 268 BUSH STREET, SUITE 3200
;      CITY: SAN FRANCISCO
;      STATE: CALIFORNIA
;      COUNTRY: USA
;      ZIP: 94104
;
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.30
;
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/306,902A
;      FILING DATE: 07-May-1999
;      CLASSIFICATION: <Unknown>
;
;      ATTORNEY/AGENT INFORMATION:
;      NAME: OSMAN, RICHARD A
;      REGISTRATION NUMBER: 36,627
;      REFERENCE/DOCKET NUMBER: UC96-217
;
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (415) 343-4341
;      TELEFAX: (415) 343-4342
;
;      INFORMATION FOR SEQ ID NO: 1:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 3014 base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: double
;      TOPOLOGY: linear
;
;      MOLECULE TYPE: cDNA
;      SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-306-902A-1

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Query Match      82.1%; Score 2259; DB 3; Length 3014;
Best Local Similarity 89.7%; Pred. No. 0;
Matches 2427; Conservative 0; Mismatches 280; Indels 0; Gaps 0;

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Qy      46 ATGGCCGTCCGGCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTC 105
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Db	361	GAATACTGGTGCCAGTGTGTGGCATGGAGCTCCTCGGGTACCACCAAAAGTCAGAAGGCC	420
Qy	466	TACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG	525
Db	421	TACATCCGGATTGCCTATTTGCGCAAGAACTTTGAGCAGGAGCCACTGGCCAAGGAAGTG	480
Qy	526	TCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGGCATCCCTCCAGCCGAG	585
Db	481	TCACTGGAGCAAGGCATTGTACTACCTTGTCGCCCCCAGAAGGAATCCCCCAGCTGAG	540
Qy	586	GTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATC	645
Db	541	GTGGAGTGGCTTCGAAATGAGGACCTCGTGGACCCCTCCCTCGATCCCAATGTGTACATC	600
Qy	646	ACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACCTACACC	705
Db	601	ACGCGGGAGCACAGCCTAGTCGTGCGTCAGGCCCGCCTGGCCGACACGGCCAACCTACACC	660
Qy	706	TGCGTGGCCAAGAACATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTTCATCGTCTAC	765
Db	661	TGTGTGGCCAAGAACATCGTAGCCCGTCGCCGAAGCACCTCTGCAGCGGTCATTGTTTAT	720
Qy	766	GTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGC	825
Db	721	GTGAACGGTGGGTGGTTCGACGTGGACTGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGT	780
Qy	826	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGGCGCTTTC	885
Db	781	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCACCTCTCAACGGGGGGCGCTTTC	840
Qy	886	TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCAGTAGACGGCAGC	945
Db	841	TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACTCTGTGCCAGTGGATGGGAGC	900
Qy	946	TGGAGCCCCTGGAGCAAGTGGTTCGGCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGT	1005
Db	901	TGGAGTTCGTGGAGTAAGTGGTCAGCCTGTGGGCTTGACTGCACCCACTGGCGGAGCCGC	960
Qy	1006	GAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGAC	1065
Db	961	GAGTGCTCTGACCCAGCACCCCGCAATGGAGGTGAGGAGTGTGGGGTGCTGACCTGGAC	1020
Qy	1066	ACCCGCAACTGTACCAAGTACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCC	1125
Db	1021	ACCCGCAACTGTACCAAGTACCTCTGCCTGCACACCGCTTCTTGCCCCGAGGACGTGGCT	1080
Qy	1126	CTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCATC	1185
Db	1081	CTCTACATCGGCCTTGTGCTGTGGCTGTGTGCCTCTTCTTGCTGTTGCTGGCCCTTGA	1140
Qy	1186	CTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTC	1245

Db	1141	CTCATTTACTGTGCGCAAGAAGGAAGGGCTGGACTCCGATGTGGCCGACTCGTCCATCCTC	1200
Qy	1246	ACCTCAGGCTTCCAGCCCCGTGAGCATCAAGCCCAGCAAAGCAGACAACCCCCCATCTGCTC	1305
Db	1201	ACCTCGGGCTTCCAGCCTGTGAGCATCAAGCCCAGCAAAGCAGACAACCCCCACCTGCTC	1260
Qy	1306	ACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG	1365
Db	1261	ACCATCCAGCCAGACCTCAGCACCACCACCTACCACCTACCAGGGCAGTCTATGTTTCGAGG	1320
Qy	1366	CAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGT	1425
Db	1321	CAGGATGGACCCAGCCCCAAGTTCCAGCTCTCTAATGGTCACCTGCTCAGCCCCACTGGGG	1380
Qy	1426	GGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCC	1485
Db	1381	AGTGGCCGCCATACGTTGCACCACAGCTCACCCACCTCTGAGGCTGAGGACTTCGTCTCC	1440
Qy	1486	CGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCGAGGCCACCAGCAACATGACCTAT	1545
Db	1441	CGCCTCTCCACCCAAACTACTTTCGTTCCTGCCCGCGGCACCAGCAACATGGCCTAC	1500
Qy	1546	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTC	1605
Db	1501	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACGGGGATCAGCCTCCTC	1560
Qy	1606	ATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG	1665
Db	1561	ATACCCCGGATGCCATCCCCCGAGGAAAGATCTACGAGATCTACCTCACACTGCACAAG	1620
Qy	1666	CCGGAAGACGTGAGGTTGCCCTTAGCTGGCTGTGAGACCCTGCTGAGTCCCATCGTTAGC	1725
Db	1621	CCAGAAGACGTGAGGTTGCCCTTAGCTGGCTGTGAGACCCTGCTGAGTCCAGTCGTTAGC	1680
Qy	1726	TGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACCTGTGGG	1785
Db	1681	TGTGGGCCCCCAGGAGTCCTGCTCACCCGGCCAGTCATCCTTGCAATGGACCACCTGTGGA	1740
Qy	1786	GAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG	1845
Db	1741	GAGCCCAGCCCTGACAGCTGGAGTCTGCGCCTCAAAAAGCAGTCCTGCGAGGGCAGTTGG	1800
Qy	1846	GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAG	1905
Db	1801	GAGGATGTGCTGCACCTTGGTGAGGAGTCACCTTCCCACCTCTACTACTGCCAGCTGGAG	1860
Qy	1906	GCCAGTGCCTGCTACGTCTTACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCC	1965
Db	1861	GCCGGGGCCTGCTATGTCTTACGGAGCAGCTGGGCCGCTTTGCCCTGGTAGGAGAGGCC	1920
Qy	1966	CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC	2025
Db	1921	CTCAGCGTGGCTGCCACCAAGCGCCTCAGGCTCCTTCTGTTTGCTCCCGTGGCCTGTACG	1980
Qy	2026	TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACCTCAAGGAG	2085
Db	1981	TCCCTTGAGTACAACATCCGAGTGTACTGCCTACACGACACCCACGACGCTCTCAAGGAG	2040





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; APPLICANT: Hink, Lindsay
; APPLICANT: Masu, Masayuki.
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1787 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-808-982-2

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Query Match          56.8%; Score 1562.4; DB 2; Length 1787;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1661; Conservative 0; Mismatches 16; Indels 9; Gaps 8;

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Db      1 GCAACTGTACCAAGTGACCTCTG-GTACACACTGCTTCTGGCCCTGAGGACGTGGCCCTCT 59

Qy      1130 ATGTGGGCTCATCGCCGTGGCCGTCTGCCTGGTCTGCTGCTGCTTGTCTCATCCTCG 1189
          |||
Db      60 ATGTGGGCTCATCGCCGTGGCCGTCTGCCTGGTCTGCTGCTGCTTGTCTCATCCTCG 119

Qy      1190 TTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCT 1249
          |||
Db      120 TTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCT 179

Qy      1250 CAGGCTTCCAGCCCGTCAGCATC-AAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACC 1308
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Db      180 CAGGCTTCCAGCCCGTCAGCATCTAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACC 239

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Qy	1309	ATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAG	1368
Db	240	ATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAG	299
Qy	1369	GATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGC	1428
Db	300	GATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGC	359
Qy	1429	GGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGC	1488
Db	360	GGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGC	419
Qy	1489	CTCTCCACCCAGAATACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGG	1548
Db	420	CTCTCCACCCAGAATACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGG	479
Qy	1549	ACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATC	1608
Db	480	ACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGAATCAGCCTCCTCATC	539
Qy	1609	CCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCG	1668
Db	540	CCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCG	599
Qy	1669	GAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGT	1728
Db	600	GAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGT	659
Qy	1729	GGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAG	1788
Db	660	GGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAG	719
Qy	1789	CCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAG	1848
Db	720	CCCAGCCCTGACAGCTGGAGCCTGGCCCTCAAAAAGCAGTCGTGCGAGGG-AGCTGGGAG	778
Qy	1849	GATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCC	1908
Db	779	GATGT-CTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCC	837
Qy	1909	AGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTC	1968
Db	838	AGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTC	897
Qy	1969	AGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCC	2028
Db	898	AGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCC	957
Qy	2029	CTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTG	2088
Db	958	CTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTG	1017
Qy	2089	GTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTC	2148
Db	1018	GTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTC-	1076
Qy	2149	AAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAG	2208

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Qy      2209 AGTAAGCTCCTTGTCTAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAG 2268
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Db      1135 AGTAAGCTCCTTGTCTAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAG 1194
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Qy      2269 CGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTCTAGCCCCAGCACTAGTGACCTGGCC 2328
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Db      1195 CGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTCTAGCCCCAGCACTAGTGACCTGGCC 1254
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Qy      2329 TGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAAC 2388
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Db      1255 TGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAAC 1314
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Qy      2389 ATCACCAAGGACACAAGGTTTGTCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCA 2448
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Db      1315 ATCACCAAGGACACAAGGTTTGTCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCA 1374
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Qy      2449 GCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCC 2508
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Db      1375 GCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCC 1434
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Qy      2509 AGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCAC 2568
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Db      1435 AGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCAC 1494
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Qy      2569 CTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAAC 2628
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Db      1495 CTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAAC 1554
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Qy      2629 CTGTGGGAGGCGCGGCACCTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCT 2688
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Db      1555 CTGTGGGAGGCGCGGCACCTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCT 1614
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Qy      2689 GGGACTGGGCCAGCCAGACGCTGGCCTC-TTCACAGTG-TCGGAGGCTGAGTGCTGAGGCC 2746
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Db      1615 GGGACTGGGCCAGCAGGACGGTGGCTTCTTTACAGTGTTTCGGAGGCTGAGTGCTGAGGCC 1674
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Qy      2747 GGCCAG 2752
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Db      1675 GGCCAG 1680

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RESULT 4

US-09-306-902A-2

; Sequence 2, Application US/09306902A

; Patent No. 6277585

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; Leonardo, E. David

; Hink, Lindsay

; Masu, Masayuki

; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

```

;      ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;      STREET: 268 BUSH STREET, SUITE 3200
;      CITY: SAN FRANCISCO
;      STATE: CALIFORNIA
;      COUNTRY: USA
;      ZIP: 94104
;
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.30
;
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/306,902A
;      FILING DATE: 07-May-1999
;      CLASSIFICATION: <Unknown>
;
;      ATTORNEY/AGENT INFORMATION:
;      NAME: OSMAN, RICHARD A
;      REGISTRATION NUMBER: 36,627
;      REFERENCE/DOCKET NUMBER: UC96-217
;
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (415) 343-4341
;      TELEFAX: (415) 343-4342
;
;      INFORMATION FOR SEQ ID NO: 2:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 1787 base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: double
;      TOPOLOGY: linear
;
;      MOLECULE TYPE: cDNA
;
;      SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-306-902A-2

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Query Match          56.8%;  Score 1562.4;  DB 3;  Length 1787;
Best Local Similarity 98.5%;  Pred. No. 0;
Matches 1661;  Conservative 0;  Mismatches 16;  Indels 9;  Gaps 8;

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Qy      1070 GCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCT 1129
          ||||||||||||||||||| ||||| |||||||||||||||||||
Db           1 GCAACTGTACCAGTGACCTCTG-GTACACACTGCTTCTGGCCCTGAGGACGTGGCCCTCT 59

Qy      1130 ATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCCTCATCCTCG 1189
          ||||||||||||||||||| ||||||||||||||||||| |||||||
Db           60 ATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCCTCATCCTCG 119

Qy      1190 TTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCT 1249
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Db           120 TTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCT 179

Qy      1250 CAGGCTTCCAGCCCGTCAGCATC-AAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACC 1308
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Db           180 CAGGCTTCCAGCCCGTCAGCATCTAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACC 239

Qy      1309 ATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAG 1368
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Db           240 ATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAG 299

Qy      1369 GATGGGCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGC 1428

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Db	300	 GATGGGCCAGCCCCAAGTTCAGCTACCAATGGGCACCTGCTCAGCCCCCTGGGTGGC	359
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Db	360	 GGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGC	419
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Qy	1549	ACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATC	1608
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Qy	1669	GAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGT	1728
Db	600	 GAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGT	659
Qy	1729	GGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAG	1788
Db	660	 GGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAG	719
Qy	1789	CCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAG	1848
Db	720	 CCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGG-AGCTGGGAG	778
Qy	1849	GATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCC	1908
Db	779	 GATGT-CTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCC	837
Qy	1909	AGTGCCTGCTACGTCTTACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTC	1968
Db	838	 AGTGCCTGCTACGTCTTACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTC	897
Qy	1969	AGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCC	2028
Db	898	 AGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCC	957
Qy	2029	CTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTG	2088
Db	958	 CTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTG	1017
Qy	2089	GTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTC	2148
Db	1018	 GTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTC-	1076
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Db	1077	 AAGGACAGTTACCACAACCT--GCCCTATCATCCACGATGTGCCAGCTCCCTGTGGAAG	1134
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; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(1282)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-833-381-1806

Query Match 42.0%; Score 1155.8; DB 4; Length 1282;  
Best Local Similarity 98.2%; Pred. No. 3e-240;  
Matches 1263; Conservative 0; Mismatches 13; Indels 10; Gaps 9;

Qy	1469	CCGAGGAGTTCGTCTCCCGCCTCTCCACCCAGAACTACTTCGCTCCCTGCCCCGAGGCA	1528
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Qy	1529	CCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATA	1588
Db	61	CCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATA	120
Qy	1589	CAGGTATCAGCCTCCTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCT	1648
Db	121	CAGGAATCAGCCTCCTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCT	180
Qy	1649	ACCTCACGCTGCACAAGCCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGC	1708
Db	181	ACCTCACGCTGCACAAGCCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGC	240
Qy	1709	TGAGTCCCATCGTTAGCTGTGGACCCCCT-GGCGTCCTGCTCACCCGGCCAGTCATCCT-	1766
Db	241	TGAGTCCCATCGTTAGCTGTGGACCCCCTGGGCGTCCTGCTCACCCGGCCAGTCATCCTG	300
Qy	1767	GGCTATGGACCACTGTGGGGAGCCCAGCCCTGACAGCT-GGAGCCTGCGCCTCAAAAAGC	1825
Db	301	GGGTATGGACCACTGTGGGGAGCCCAGCCCTGACAGCTGGGAGCCTGCGCCTCAAAAAGC	360
Qy	1826	AGTCGTGCGAGGGCAGCTGGGAGGATGTGC-TGCACCTGGGCGAGGAGGCGCCCTCCCAC	1884
Db	361	AGTCGTGCGAGGGCAGCTGGGAGGATGTGCTTGCACCTGGGCGAGGAGGCGCCCTCCCAC	420
Qy	1885	CTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCGCG	1944
Db	421	CTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGAGCGCG	480
Qy	1945	TTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTG	2004
Db	481	TATGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTG	540
Qy	2005	TTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGAC	2064
Db	541	TTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACATACTGGTCTACTGCCTGCATGAC	600
Qy	2065	ACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATC	2124
Db	601	ACTCACGATGCACTCAACGTAGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATC	660
Qy	2125	CAGGAGCCACGGGTCCTGCACTTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCAC	2184
Db	661	CAGGAGCCACGGGTCCTGCACTTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCAC	720

Qy 2185 GATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTTGTTCAGCTACCAGGAGATCCCCTTT 2244  
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 Db 721 GATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTTGTTCAGCTACCAGGAGATCCCCTTT 780

Qy 2245 TATCACATCTGGAATGGCACGCAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTC 2304  
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 Db 781 TATCACATCTGGAATGGCACGCAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTC 840

Qy 2305 AGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGG 2364  
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 Db 841 AGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGG 900

Qy 2365 CAGAGCTTCAGCATCAACTTCAACATCACCAGGACACAAGGTTTGCTGAGCTGCTGGCT 2424  
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 Db 901 CAGAGCTTCAGCATCAACTTCAACATCACCAGGACACAAGGTTTGCTGAGCTGCTGGCT 960

Qy 2425 CTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTC 2484  
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 Db 961 CTGGAGAGTGAAGCGNGGGTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTC 1020

Qy 2485 CTCATTCGGCAGAAGATAA-TTTCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTG 2543  
 |||  
 Db 1021 CTCATTCGGCAGAAGATAATTTTCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTG 1080

Qy 2544 GCGG-ACTCTGGCCCAGAACTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGC 2602  
 |||  
 Db 1081 GCGGAACTCTGGCCCAGAACTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGC 1140

Qy 2603 CCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACC 2662  
 |||  
 Db 1141 CCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACC 1200

Qy 2663 TCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAG 2722  
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 Db 1201 TCAGCCAGCTGG-TGCAGCAGTGGCTGGACTGGGC--AGCAGACGCTGG-CTCTTCACAG 1256

Qy 2723 TGTCGGAGGCTGAGTGCTGAGGCCGG 2748  
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 Db 1257 TGTCGGAGGCTGAGTGCTGAGGCCGG 1282

RESULT 6

US-08-808-982-3

; Sequence 3, Application US/08808982

; Patent No. 5939271

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; APPLICANT: Leonardo, E. David

; APPLICANT: Hink, Lindsay

; APPLICANT: Masu, Masayuki

; APPLICANT: Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200



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;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94104
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/808,982
;      FILING DATE:
;      CLASSIFICATION:  530
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  OSMAN, RICHARD A
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  UC96-217
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 343-4341
;      TELEFAX:  (415) 343-4342
;      INFORMATION FOR SEQ ID NO:  3:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  2831 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  cDNA
US-08-808-982-3

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Query Match          30.6%;  Score 841.4;  DB 2;  Length 2831;
Best Local Similarity 60.0%;  Pred. No. 2.4e-172;
Matches 1638;  Conservative  0;  Mismatches  961;  Indels  130;  Gaps  9;

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Qy      143  ACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCAGGATG 202
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Db      104  ACTCCTTCCCATCAGCACCCGCGGAGCAGCTGCCTCACTTCCTGCTGGAACCAGAGGATG 163

Qy      203  TGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGA 262
        || || || || || || || || || || || || || || || || || || || ||
Db      164  CCTACATCGTAAAGAACAAGCCAGTGGAATTGCACTGCCGAGCCTTCCCTGCCACACAGA 223

Qy      263  TCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCA 322
        || | || || || || || || || || || || || || || || || || || ||
Db      224  TCTACTTCAAGTGTAATGGCGAGTGGGTTAGCCAGAAAGGCCACGTACGCAGGAGAGCC 283

Qy      323  CAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGG 382
        || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      284  TGGATGAGGCCACAGGCTTGCGAATACGAGAGGTGCAGATAGAGGTGTCGCGGCAGCAGG 343

Qy      383  TCGAGAAGGTGTTCTGGGCTGGAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGG 442
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      344  TGGAGGAACCTTTTGGGCTCGAGGACTACTGGTGTGTCAGTGCGTGGCCTGGAGCTCTTCGG 403

Qy      443  GCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGC 502
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      404  GAACCACCAAGAGTCGCGGAGCCTACATCCGCATTGCCTACTTGCGCAAGAACTTTGACC 463

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Qy 503 AGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCAC 562  
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 Db 464 AGGAGCCTCTGGCGAAGGAGGTACCCTTGGATCATGAGGTCTTCTGCAGTGCCGCCAC 523

Qy 563 CGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGT 622  
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 Db 524 CAGAGGGAGTGCCTGTGGCTGAGGTGGAATGGCTCAAGAATGAAGATGTCATCGATCCCG 583

Qy 623 CCCTGGACCCCAATGTATACATCACGCGGGAGCACAGCCTGGTGGTGGCAGAGCCCGCC 682  
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 Db 584 CTCAGGACACTAACTTCCTGCTCACCATTGACCACAACCTCATCATCCGCCAGGCGCGCC 643

Qy 683 TTGCTGACACGGCCAATACTACACCTGCGTGGCCAAGAATCGTGGCAGCTCGCCGACGCG 742  
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 Db 644 TCTCAGACACAGCCAATACTACACCTGTGTGGCAAAGAATATTGTGGCCAAGCGCCGGAGCA 703

Qy 743 CCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGGTGCAGCTGGACCGAGTGGTCCG 802  
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 Db 704 CGACGGCCACAGTCATCGTCTATGTGAACGGAGGTTGGTCCAGCTGGGCAGAAATGGTCAC 763

Qy 803 TCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGG 862  
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 Db 764 CCTGCTCTAACCCTGCGGCCGAGGTTGGCAGAAACGTACTAGGACCTGCACCAACCCAG 823

Qy 863 CGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCA 922  
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 Db 824 CCCCCTCAATGGAGGTGCCTTCTGCGAGGGACAGGCTTGCCAGAAGACGGCTTGACCA 883

Qy 923 CCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTGGCCCTGTGGGCTGG 982  
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 Db 884 CCGTGTGCCCAGTGGATGGAGCGTGGACTGAGTGGAGCAAGTGGTCCGCCTGCAGCACAG 943

Qy 983 ACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGG 1042  
 | || | ||||| ||||| ||||| | || | |||| ||||| ||||| |||||  
 Db 944 AGTGTGCGCACTGGCGCAGCCGCGAGTGCATGGCACC CGCGCCCAAGACGGAGGCCGTG 1003

Qy 1043 AGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTG 1102  
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 Db 1004 ACTGCAGCGGGACGCTACTTGACTCCAAGAACTGCACCGATGGGCTGTGCGTGTGAATC 1063

Qy 1103 CTTCTGGCC-----CTGAGGACGTGGCCCTCT 1129  
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 Db 1064 AGAGAACTCTAAACGACCCTAAAAGCCGCCCTGGAGCCGTGCGGAGACGTGGCGCTGT 1123

Qy 1130 ATGTGGGCCTC---ATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGTCTCTCATCC 1186  
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 Db 1124 ATGCGGGCCTCGTGGTGGCCGTCTTTGTGGTCTGGCAGTTCTCATGGCTGTAGGAGTGA 1183

Qy 1187 TCGTTTATTGCCGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATT---C 1243  
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 Db 1184 TCGTGTACCGGAGAACTGCCGGGACTTCGACACGGACATCACTGACTCCTCTGCTGCC 1243

Qy 1244 TCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCAGCAAAGCAGACAACCCCCATCTGC 1303  
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 Db 1244 TCACTGGTGGTTTCCACCCCGTCAACTTCAAGACTGCAAGGCCAGCAACCCACAGCTCC 1303

Qy 1304 T-----CACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCT 1357

Db	1304	TGCACCCATCCGCCCTCCGGACCTAACGGCCAGTGCTGGCATCTACCGCGGACCTGTGT	1363
Qy	1358	GTCCCCGGCAGGA-----TG	1372
Db	1364	ATGCCCTGCAGGACTCTGCCGACAAGATCCCTATGACTAATTCACCCCTTCTGGATCCCT	1423
Qy	1373	GGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCC-----CCTGG	1423
Db	1424	TGCCCAGCCTCAAGATCAAGGTCTATGACTCCAGCACCATCGGCTCTGGGGCTGGCCTGG	1483
Qy	1424	GTGGCGGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCT	1483
Db	1484	CTGATGGAGCCGACCTGCTGGGTGTCTTACCACCCGGTACATACCCAGGCGATTTCTCCC	1543
Qy	1484	CCCGCCTCTCCACCCAGAAC-----TACTTCCGCTCCC	1516
Db	1544	GGGACACCCACTTCCTGCACCTGCGCAGCGCCAGCCTTGGTTCACGACCTCCTGGGCC	1603
Qy	1517	TGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGA	1576
Db	1604	TCCCTCGAGACCCAGCAGCAGTGTGAGTGGCACCTTTGGTTGCCCTGGGTGGGAGGCTGA	1663
Qy	1577	TGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCCATACCCGAGGGAAGA	1636
Db	1664	CCATTCCCGGCACAGGGGTGACGCTGTTGGTACCAAATGGAGCCATTCCCCAGGGCAAGT	1723
Qy	1637	TCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGGTTGCCCTAGCTGGCT	1696
Db	1724	TCTATGACTTGTATCTACGTATCAACAAGACTGAAAGCACCTCCCACTTTCGGAAGGTT	1783
Qy	1697	GTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCTGGCGTCTGCTCACCCGGC	1756
Db	1784	CCCAGACAGTATTGAGCCCCCTCGGTGACCTGCGGGCCACGGGCCTCCTCCTGTGCCGCC	1843
Qy	1757	CAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGACAGCTGGAGCCTGCGCC	1816
Db	1844	CTGTTGTCTCACTGTGCCCCACTGTGCTGAAGTCATTGCCGGAGACTGGATCTTCCAGC	1903
Qy	1817	TCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGC	1876
Db	1904	TCAAGACCCAGGCCCATCAGGGCCACTGGGAGGAGGTGGTGACTTTGGATGAGGAGACTC	1963
Qy	1877	CCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTACCGAGCAGC	1936
Db	1964	TGAACACCCCTGCTACTGCCAGCTAGAGGCTAAATCCTGCCACATCCTGTTGGACCAGC	2023
Qy	1937	TGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGC	1996
Db	2024	TGGGTACCTACGTGTTACGGGCGAGTCCTACTCCCGCTCCGCAGTCAAGCGGCTCCAGC	2083
Qy	1997	TGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCC	2056
Db	2084	TAGCCATCTTCGCCCCAGCCCTCTGCACCTCCCTGGAGTATAGTCTCAGGGTCTACTGTC	2143
Qy	2057	TGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGAC	2116





Db 344 TGGAGGAAC TTTTGGGCTCGAGGACTACTGGTGT CAGTGC GTGGCCTGGAGCTCTTCGG 403  
 Qy 443 GCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGC 502  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 404 GAACCACCAAGAGTCGCGGAGCCTACATCCGCATTGCCTACTTGC GCAAGAACTTTGACC 463  
 Qy 503 AGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCAC 562  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 464 AGGAGCCTCTGGCGAAGGAGGTACCCTTGGATCATGAGGTCCTTCTGCAGTGCCGCCAC 523  
 Qy 563 CGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGAGACCCGT 622  
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 Db 524 CAGAGGGAGTGCCTGTGGCTGAGGTGGAATGGCTCAAGAATGAAGATGTCATCGATCCCG 583  
 Qy 623 CCCTGGACCCCAATGTATACATCACGCGGGAGCACAGCCTGGTGGTGC GACAGGCCCGCC 682  
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 Db 584 CTCAGGACACTAACTTCTGCTCACCATTGACCACAACCTCATCATCCGCCAGGCGCGCC 643  
 Qy 683 TTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAACATCGTGGCACGTGCGCCGAGCG 742  
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 Db 644 TCTCAGACACAGCCAACTACACCTGTGTGGCAAAGAATATTGTGGCCAAGCGCCGGAGCA 703  
 Qy 743 CCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGGTGCAGCTGGACCGAGTGGTCCG 802  
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 Db 704 CGACGGCCACAGTCATCGTCTATGTGAACGGAGGTTGGTCCAGCTGGGCAGAATGGTCAC 763  
 Qy 803 TCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGG 862  
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 Db 764 CCTGCTCTAACCCTGCGGCCGAGGTTGGCAGAAACGTACTAGGACCTGCACCAACCCAG 823  
 Qy 863 CGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCA 922  
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 Db 824 CCCCCTCAATGGAGGTGCCTTCTGCGAGGGACAGGCTTGCCAGAAGACGGCTTGACCA 883  
 Qy 923 CCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTCCGCCCTGTGGGCTGG 982  
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 Db 884 CCGTGTGCCCAGTGGATGGAGCGTGGACTGAGTGGAGCAAGTGGTCCGCCCTGCAGCACAG 943  
 Qy 983 ACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGG 1042  
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 Db 944 AGTGTGCGCACTGGCGCAGCCGCGAGTGCATGGCACC GCCGCCAGAACGGAGGCCGTG 1003  
 Qy 1043 AGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTG 1102  
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 Db 1004 ACTGCAGCGGGACGCTACTTGACTCCAAGAACTGCACCGATGGGCTGTGCGTGCTGAATC 1063  
 Qy 1103 CTTCTGGCC-----CTGAGGACGTGGCCCTCT 1129  
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 Db 1064 AGAGAACTCTAAACGACCCTAAAAGCCGCCCCCTGGAGCCGTGCGGAGACGTGGCGCTGT 1123  
 Qy 1130 ATGTGGGCCTC---ATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCCTCATCC 1186  
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 Db 1124 ATGCGGGCCTCGTGGTGGCCGTCTTTGTGGTTCTGGCAGTTCTCATGGCTGTAGGAGTGA 1183  
 Qy 1187 TCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATT---C 1243  
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 Db 1184 TCGTGTACCGGAGAACTGCCGGGACTTCGACACGGACATCACTGACTCCTCTGCTGCC 1243

Qy	1244	TCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCATCTGC	1303
Db	1244	TCACTGGTGGTTTCCACCCCGTCAACTTCAAGACTGCAAGGCCAGCAACCCACAGCTCC	1303
Qy	1304	T-----CACCATCCAGCCGGACCTCAGCACCACCACCACCTACCAGGGCAGTCTCT	1357
Db	1304	TGCACCCATCCGCCCTCCGGACCTAACGGCCAGTGCTGGCATCTACCGCGGACCTGTGT	1363
Qy	1358	GTCCCCGGCAGGA-----TG	1372
Db	1364	ATGCCCTGCAGGACTCTGCCGACAAGATCCCTATGACTAATTACCCCTTCTGGATCCCT	1423
Qy	1373	GGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCC-----CCTGG	1423
Db	1424	TGCCCAGCCTCAAGATCAAGGTCTATGACTCCAGCACCATCGGCTCTGGGGCTGGCCTGG	1483
Qy	1424	GTGGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCT	1483
Db	1484	CTGATGGAGCCGACCTGCTGGGTGTCTTACCACCCGGTACATAACCAGGCGATTCTCCC	1543
Qy	1484	CCCGCCTCTCCACCCAGAAC-----TACTTCCGCTCCC	1516
Db	1544	GGGACACCCACTTCTGCACCTGCGCAGCGCCAGCCTTG GTTCCAGCACCTCCTGGGCC	1603
Qy	1517	TGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGA	1576
Db	1604	TCCCTCGAGACCCAGCAGCAGTGT CAGTGGCACCTTTGGTTGCCTGGGTGGGAGGCTGA	1663
Qy	1577	TGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCCATACCCCGAGGGAAGA	1636
Db	1664	CCATTCCCGGCACAGGGGTGAGCCTGTTGGTACCAAATGGAGCCATTCCCCAGGGCAAGT	1723
Qy	1637	TCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGGTTGCCCTTAGCTGGCT	1696
Db	1724	TCTATGACTTGTATCTACGTATCAACAAGACTGAAAGCACCCCTCCCACTTTCGGAAGGTT	1783
Qy	1697	GTCAGACCCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCTGGCGTCCTGCTCACCCGGC	1756
Db	1784	CCCAGACAGTATTGAGCCCCTCGGTGACCTGCGGGGCCACGGGCC'TCCTCCTGTGCCGCC	1843
Qy	1757	CAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGACAGCTGGAGCCTGCGCC	1816
Db	1844	CTGTTGTCT'CACTGTGCCCCACTGTGCTGAAGTCATTGCCGGAGACTGGATCTTCCAGC	1903
Qy	1817	TCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGC	1876
Db	1904	TCAAGACCCAGGCCCATCAGGGCCACTGGGAGGAGGTGGTGACTTTGGATGAGGAGACTC	1963
Qy	1877	CCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGC	1936
Db	1964	TGAACACCCCTGCTACTGCCAGCTAGAGGCTAAATCCTGCCACATCCTGTTGGACCAGC	2023
Qy	1937	TGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGC	1996
Db	2024	TGGGTACCTACGTGTTACGGGCGAGTCCTACTCCCCTCCGAGTCAAGCGGCTCCAGC	2083





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; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1807
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1605)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1807
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Query Match          15.7%; Score 432; DB 4; Length 1605;
Best Local Similarity 62.5%; Pred. No. 4e-84;
Matches 737; Conservative 0; Mismatches 435; Indels 7; Gaps 4;
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Qy      1515 CCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCT 1574
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Db      421 CCTGCCCCGAGACCCAGGGAGCAGCGTCAGCGGCACCTTTGGCTGCCTGGGTGGGAGGCT 480

Qy      1575 GATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCCATACCCCGAGGGAA 1634
          | ||||| ||||| ||||| | || | || | | ||||| |||| | | |
Db      481 CANCATCCCCGGCACAGGGGTGAGCTTGTGGTGCCCAATGGAGCCATTCCCCAGGGCAA 540

Qy      1635 GATCTATGA--GATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGGTTGCCCTAGCT 1692
          | |||| | | | | | | | | | | | | | | | | | | | |
Db      541 GTTCTACGAAGATGTATTCTACTCATCAACAAGGCAGAAAGTACCCTCCCGCTTTCAGAA 600

Qy      1693 GGCTGTGCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCTGGCGTCCTGCTCACC 1752
          || || || | | |||| || | ||||| || | ||||| || | |
Db      601 GGGACCCANACAGTATTGAGCCCCCTCGGTGACCTGTGGACCCACAGGCCTCCTGCTGTGC 660

Qy      1753 CGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGACAGCTGGAGCCTG 1812
          || || ||||| || | || | ||||| || | || | | | |||| | |
Db      661 CGCCCCGTCATCCTCACCATGCCCCACTGTGCCGAAGTCAGTGCCCGTGACTGGATCTTT 720

Qy      1813 CGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAG 1872
          | |||| | | | | | | ||||| || || | | |||| | ||||
Db      721 CAGCTCAAGACCCAGGCCACCAGGGCCACTGGGANGAGGTGGTGACCCTGGATGAGGAG 780

Qy      1873 GCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAG 1932
          | | | | | | ||||| ||||| |||| | | | | | | | |
Db      781 ACCCTGAACACACCCTGCTACTGCCAGCTGGAGCCCAGGGCCTGTACATCCTGCTGGAC 840

Qy      1933 CAGCTGGGCGCGCT-TTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCT 1991
          ||||| || | | | |||| || | | | | | | | | | | | |
Db      841 CAGCTGGGCACCTACCGTGTTCACGGGCGAGTCCTATTCCCGCTCAGCAGTCAAGCGGCT 900

Qy      1992 CAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTA 2051
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Db 901 CCAGCTGGCCGTCTTCGCCCCCGCCCTCTGCACCTCCCTGGAGTACAGCCTCCGGGTCTA 960  
 Qy 2052 CTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGG 2111  
 Db 961 CTGCCTGGAGGACACGCCTGTAGCACTGAAGGAGGTGCTGGAGCTGGAGCGGACTCTGGG 1020  
 Qy 2112 GGGACAGCTGATCCAGGAGCCACGGGTCTTGCACTTCAAGGACAGTTACCACAACCTGCG 2171  
 Db 1021 CGGATACTTGGTGGAGGAGCCGAAACCGCTAATGTTCAAGGACAGTTACCACAACCTGCG 1080  
 Qy 2172 CCTATCCATCCACGATGTGCCCAGCTCCCCTGTGGAAGAGTAAGCTCCTTGTGAGCTACCA 2231  
 Db 1081 CCTCTCCCTCCATGACCTCCCCCATGCCATTGGAGGAGCAAGCTGCTGGCCAAAATACCA 1140  
 Qy 2232 GGAGATCCCTTTTATCACATCTGGAATGGCAGCGAGCGGTACTTGCACTGCACCTTCAC 2291  
 Db 1141 GGAGATCCCTTCTATCACATTTGGAGTGGCAGCCAGAAGGCCCTCCACTGCACTTTCAC 1200  
 Qy 2292 CCTGGAGCGTGTGAGCCCCAG-CACTAGTGACCTGGCCTGCAAGCTGTGGGTGTGGCAGG 2350  
 Db 1201 CCTGGAGAGGCACAGGCTTGGCCTCCACAGAGCTCACCTGCAAGATCTGCGTGCGGCAAG 1260  
 Qy 2351 TGGAGGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAG---GACACAAGGT 2407  
 Db 1261 TGGAAGGGGAGGGCCAGATATTCCAGCTGCATACCACTCTGGCAGAGACACCTGCTGGCT 1320  
 Qy 2408 TTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGCCCCAGTG 2467  
 Db 1321 CCCTGGACACTCTCTGCTCTGCCCTGGCAGCACTGTCACCACCCAGCTGGGACCTTATG 1380  
 Qy 2468 CCTTCAAGATCCCCTTCCCTCATTCGGCAGAAGATAAATTTCCAGCCTGGACCCACCCTGTA 2527  
 Db 1381 CCTTCAAGATCCCACTGTCCATCCGCCAGAAGATATGCAACAGCCTAGATGCCCCCAACT 1440  
 Qy 2528 GGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAGCCATCTCAGCT 2587  
 Db 1441 CACGGGGCAATGACTGGCGGATGTTAGCACAGAAGCTCTCTATGGACCGGTACCTGAATT 1500  
 Qy 2588 TCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCGCGGCACT 2647  
 Db 1501 ACTTTGCCACCAAAGCGAGCCCCACGGNTGTGATCCTGGACCTCTGGGAAGCTCTGCAGC 1560  
 Qy 2648 TCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGG 2686  
 Db 1561 AGGACGATGGGGACCTCAACAGCCTGNCGAGTGCCTTGG 1599

US-08-253-155A-17/c

```

;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: LAHIVE & COCKFIELD
;   STREET: 60 State Street
;   CITY: Boston
;   STATE: MA
;   COUNTRY: USA
;   ZIP: 02109
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: ASCII(text)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/253,155A
;   FILING DATE: 02-JUN-1994
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Vincent, Matthew P.
;   REGISTRATION NUMBER: 36,709
;   REFERENCE/DOCKET NUMBER: MII-028
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (617) 227-7400
;   TELEFAX: (617) 227-5941
;   INFORMATION FOR SEQ ID NO: 17:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 771 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
US-08-253-155A-17

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Query Match          9.8%; Score 269; DB 1; Length 771;
Best Local Similarity 67.6%; Pred. No. 4.6e-49;
Matches 406; Conservative 1; Mismatches 191; Indels 3; Gaps 2;

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Qy      1700 AGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCTGGCGTCCTGCTCACCCGGCCAG 1759
        |||| | |||| || | | ||||| || | || ||||| || || |
Db      738 AGACAGTATTGAGCCCCTCGGTGACCTGTGGACCCACAGGCCTCCTGCTGTGCCGCCCCG 679

Qy      1760 TCATCCTGGCTATGGACCACTGTGGGGAGCCAGCCCTGACAGCTGGAGCCTGCGCCTCA 1819
        ||||| | || | ||||| || || | |||| | | | ||||
Db      678 TCATCCTCACCATGCCCCACTGTGCCGAAGTCAGTGCCCGTGACTGGATCTTTCAGCTCA 619

Qy      1820 AAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCT 1879
        | | ||| | | |||| | ||||| || | | |||| | |||| | |
Db      618 AGACCCAGGCCCCACCAGGGCCACTGGGAGGAGGTGGTGACCTGGATGAGGAGACCCTGA 559

Qy      1880 CCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGG 1939
        | | || ||||| ||||| |||| || || | || |||||
Db      558 ACACACCCTGCTACTGCCAGCTGGAGCCCAGGGCCTGTACATCCTGCTGGACCAGCTGG 499

Qy      1940 GCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGC 1999
        || || | | ||| ||| | | | || | ||||| :|| |||||
Db      498 GCACCTACGTGTTACGGGCGAGTCCTATTCCCGCTCAGCAGTCAAGCGGSTCCAGCTGG 439

Qy      2000 TTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGC 2059

```

[illegible]

US-08-808-982-4

; Patent No. 5939271

```
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsay
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
```

```

;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:     IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:     PatentIn Release #1.0, Version #1.30

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; APPLICATION NUMBER: US/08/808,982

; CLASSIFICATION: 530

NAME: OSMAN, RICHARD A

; REFERENCE/DOCKET NUMBER: UC96-217

; TELEPHONE: (415) 343-4341  
 ; TELEFAX: (415) 343-4342  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 305 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 US-08-808-982-4

Query Match 4.3%; Score 119; DB 2; Length 305;  
 Best Local Similarity 68.1%; Pred. No. 7.8e-17;  
 Matches 209; Conservative 0; Mismatches 95; Indels 3; Gaps 3;

Qy 1862 TGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACG 1921  
 ||| ||||| | | | | | ||||| ||||| ||| ||| |||  
 Db 1 TGGATGAGGAGACCCTGAACACACCCTGCTACTG-CAGCTGGAGCCCAGGGCCTG-TACA 58  
 Qy 1922 TCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCG 1981  
 || | || ||||| || | | || || | | | | | |||  
 Db 59 TCCTGCTGGACCAGCTGGGCACCTACGTTTTTCACGGGCGAGTCCTATTCCTGCTCAGCAG 118  
 Qy 1982 CCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACA 2041  
 ||||| || |||| | || || | | ||||| ||||| ||||| |  
 Db 119 TCAAGCGGCTCCAGCTGGCCGT-TTCGCCCCGCCCTCTGCACCTCCCTGGAGTACAGCC 177  
 Qy 2042 TCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGA 2101  
 ||||| ||||| || |||| | | |||| ||||| || ||||| ||  
 Db 178 TCCGGGTCTACTGCCTGGAGGACACGCCTGTAGCACTGAAGGAGGTGCTGGAGCTGGAGC 237  
 Qy 2102 AGCAGCTGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTCAAGGACAGTTACC 2161  
 | |||| || | || | |||| | | ||||| ||||| |||||  
 Db 238 GGA CTCTGGGCGGATACTTGGTGGAGGAGCCGAAACCGCTAATGTTCAAGGACAGTTACC 297  
 Qy 2162 ACAACCT 2168  
 |||||  
 Db 298 ACAACCT 304

RESULT 11

US-09-306-902A-4

; Sequence 4, Application US/09306902A  
 ; Patent No. 6277585  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tessier-Lavigne, Marc  
 ; Leonardo, E. David  
 ; Hink, Lindsay  
 ; Masu, Masayuki  
 ; Kazuko, Keino-Masu  
 ; TITLE OF INVENTION: Netrin Receptors  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
 ; STREET: 268 BUSH STREET, SUITE 3200  
 ; CITY: SAN FRANCISCO  
 ; STATE: CALIFORNIA

```

;          COUNTRY: USA
;          ZIP: 94104
;    COMPUTER READABLE FORM:
;          MEDIUM TYPE: Floppy disk
;          COMPUTER: IBM PC compatible
;          OPERATING SYSTEM: PC-DOS/MS-DOS
;          SOFTWARE: PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/09/306,902A
;          FILING DATE: 07-May-1999
;          CLASSIFICATION: <Unknown>
;    ATTORNEY/AGENT INFORMATION:
;          NAME: OSMAN, RICHARD A
;          REGISTRATION NUMBER: 36,627
;          REFERENCE/DOCKET NUMBER: UC96-217
;    TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (415) 343-4341
;          TELEFAX: (415) 343-4342
;    INFORMATION FOR SEQ ID NO: 4:
;          SEQUENCE CHARACTERISTICS:
;            LENGTH: 305 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;          MOLECULE TYPE: cDNA
;          SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-306-902A-4

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Query Match          4.3%;  Score 119;  DB 3;  Length 305;
Best Local Similarity 68.1%;  Pred. No. 7.8e-17;
Matches 209;  Conservative 0;  Mismatches 95;  Indels 3;  Gaps 3;

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Qy      1862 TGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACG 1921
          ||| ||||| | | | | | || ||||| ||||| ||| ||| |||
Db          1 TGGATGAGGAGACCCTGAACACACCCTGCTACTG-CAGCTGGAGCCCAGGGCCTG-TACA 58

Qy      1922 TCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCG 1981
          || | || ||||| || | | ||| ||| | | | |
Db          59 TCCTGCTGGACCAGCTGGGCACCTACGTTTTCACGGGCGAGTCCTATTCCCGCTCAGCAG 118

Qy      1982 CCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACA 2041
          ||||| ||| |||| | || || || | ||||| ||||| |
Db          119 TCAAGCGGCTCCAGCTGGCCGT-TTCGCCCCCGCCCTCTGCACCTCCCTGGAGTACAGCC 177

Qy      2042 TCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGA 2101
          ||||| ||||| || |||| | | |||| ||||| || |||||
Db          178 TCCGGGTCTACTGCCTGGAGGACACGCCTGTAGCACTGAAGGAGGTGCTGGAGCTGGAGC 237

Qy      2102 AGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTCAAGGACAGTTACC 2161
          | |||| ||| | || | ||||| || ||||| |||||
Db          238 GGACTCTGGGCGGATACTTGGTGGAGGAGCCGAAACCGCTAATGTTCAAGGACAGTTACC 297

Qy      2162 ACAACCT 2168
          |||||
Db          298 ACAACCT 304

```

RESULT 12

US-08-985-526-2

; Sequence 2, Application US/08985526

; Patent No. 6080728

; GENERAL INFORMATION:

; APPLICANT: Mixson, James A

; TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA

; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN

GENE

; TITLE OF INVENTION: THERAPY

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Connolly, Bove, Lodge, & Hutz

; STREET: 1220 Market Street, P.O. Box 2207

; CITY: Wilmington

; STATE: Delaware

; COUNTRY: U.S.A.

; ZIP: 19899

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/985,526

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/608,845

; FILING DATE: 16-JUL-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: McMorrow Jr., Robert G

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (302) 658-9141

; TELEFAX: (302) 658-5613

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 657 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-985-526-2

Query Match 1.9%; Score 53.6; DB 3; Length 657;

Best Local Similarity 52.7%; Pred. No. 0.012;

Matches 116; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

Qy 756 CATCGTCTACGTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAG 815  
 || || || | | ||| ||| |||| | ||| ||||| || || | ||

Db 222 CAGCGACTCTGCGGACGATGGCTGGTCTCCATGGTCCGAGTGGACCTCCTGTTCTACGAG 281

Qy 816 CTGTGGGCGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGG 875  
 ||||| || ||| | || |||| |||| | || | || |

Db 282 CTGTGGCAATGGAATTCAGCAGCGCGGCCGCTCCTGCGATAGCCTCAACAACCGATGTGA 341

Qy 876 GGGCGCTTTCTGTGAGGGGCAGAAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCAGT 935  
 |||| | | || | || ||| | | || | || | |

```

Db          342 GGGCTCCTCGGTCCAGACACGGACCTGCCACATTCAGGAGTGTGACAAAAGATTTAAACA 401
Qy          936 AGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGT 975
              || || ||||| ||| | ||||| | |||
Db          402 GGATGGTGGCTGGAGCCACTGGTCCCCGTGGTCATCTTGT 441

```

RESULT 13

US-08-985-526-4

; Sequence 4, Application US/08985526

; Patent No. 6080728

; GENERAL INFORMATION:

; APPLICANT: Mixson, James A

; TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA

; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN

GENE

; TITLE OF INVENTION: THERAPY

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Connolly, Bove, Lodge, & Hutz

; STREET: 1220 Market Street, P.O. Box 2207

; CITY: Wilmington

; STATE: Delaware

; COUNTRY: U.S.A.

; ZIP: 19899

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/985,526

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/608,845

; FILING DATE: 16-JUL-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: McMorrow Jr., Robert G

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (302) 658-9141

; TELEFAX: (302) 658-5613

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1326 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-985-526-4

Query Match 1.9%; Score 53.6; DB 3; Length 1326;

Best Local Similarity 52.7%; Pred. No. 0.015;

Matches 116; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

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Qy          756 CATCGTCTACGTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAG 815
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Db          222 CAGCGACTCTGCGGACGATGGCTGGTCTCCATGGTCCGAGTGGACCTCCTGTTCTACGAG 281

```



Qy 816 CTGTGGGCGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGG 875  
 ||||| || ||| || ||| ||| || |  
 Db 282 CTGTGGCAATGGAATTCAGCAGCGCGGCCGCTCCTGCGATAGCCTCAACAACCGATGTGA 341  
 Qy 876 GGGCGCTTTCTGTGAGGGGCGAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGT 935  
 |||| | | || | || ||| | || | || |  
 Db 342 GGGCTCCTCGGTCCAGACACGGACCTGCCACATTCAGGAGTGTGACAAAAGATTAAACA 401  
 Qy 936 AGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGT 975  
 || || ||||| || | |||| | ||  
 Db 402 GGATGGTGGCTGGAGCCACTGGTCCCCGTGGTCATCTTGT 441

RESULT 14

US-09-252-991A-7947

; Sequence 7947, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 7947

; LENGTH: 699

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-7947

Query Match 1.9%; Score 52.8; DB 4; Length 699;

Best Local Similarity 47.6%; Pred. No. 0.019;

Matches 156; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

Qy 1824 GCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCCCTCCCA 1883  
 || | || ||| | | | | || | || | || | || | || |  
 Db 160 GCCGAAGTACGACGTCTACGACAGCAACGAGGTGCTCGAGGCCAAGCTGCTGTCCGGGCA 219  
 Qy 1884 CCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCG 1943  
 | |||| || | ||| | |||| | || | || | || | || |  
 Db 220 TTCCGGCTACGACCTGGTGGTGCCAGCGACAGCTTCCTGCCCAACTACCTGAAGGCCGA 279  
 Qy 1944 CTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCT 2003  
 | || | | || || || | || | || | || |||| | || ||  
 Db 280 GGTGTTCCAGCCGCTGGACAAGAGCAAGCTGCCGAAGTGAAGAACCTCAACCCGGCCCT 339  
 Qy 2004 GTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGA 2063  
 | | | | |||| || || || | | | | || || |  
 Db 340 GCTCAAGGTGCTCGCCGGCAAGGACCCCGGCAACCGCTACGTGATGCCCTACATGTGGGG 399

```

Qy      2064 CACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGAT 2123
          |||| |||      | | | | | | || |      | ||| || | | | | |
Db      400 CACCAACGGCATCGCCTACAACCTCGACAAGGTCCGCGCGGTGCTCGGCGACGATGCGCC 459

Qy      2124 CCAGGAGCCACGGGTCCTGCACTTCAAG 2151
          | ||| | ||| |||| | |||||
Db      460 GCTGGACTCCTGGGACCTGGTGTTCAG 487

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# RESULT 15

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US-09-252-991A-7809
; Sequence 7809, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7809
; LENGTH: 1302
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7809

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Query Match          1.9%; Score 52.8; DB 4; Length 1302;
Best Local Similarity 47.6%; Pred. No. 0.022;
Matches 156; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

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Qy      1824 GCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCA 1883
          || | || ||| | | | | | | || | || | | | | | ||
Db      360 GCCGAAGTACGACGTCTACGACAGCAACGAGGTGCTCGAGGCCAAGCTGCTGTCCGGGCA 419

Qy      1884 CCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGGCCG 1943
          | |||| || | ||| | |||| | | ||| | | || | | | | || |
Db      420 TTCCGGCTACGACCTGGTGGTGCCAGCGACAGCTTCCTGCCCAACTACCTGAAGGCCGA 479

Qy      1944 CTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCT 2003
          | || | | || || || || | | || | ||||| | | ||
Db      480 GGTGTTCCAGCCGCTGGACAAGAGCAAGCTGCCGAAC TGGAAGAACCTCAACCCGGCCCT 539

Qy      2004 GTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGA 2063
          | | | | | ||| ||| || || || | | | | || | || |
Db      540 GCTCAAGGTGCTCGCCGGCAAGGACCCCGGCAACCGCTACGTGATGCCCTACATGTGGGG 599

Qy      2064 CACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGAT 2123
          |||| |||      | | | | | | || |      | ||| || | | | |
Db      600 CACCAACGGCATCGCCTACAACCTCGACAAGGTCCGCGCGGTGCTCGGCGACGATGCGCC 659

Qy      2124 CCAGGAGCCACGGGTCCTGCACTTCAAG 2151

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Db                   | | | | | | | | | |  
660 GCTGGACTCCTGGGACCTGGTGTCAAG 687

Search completed: July 7, 2004, 16:24:16  
Job time : 190 secs

OM nucleic - nucleic search, using sw model

Run on: July 7, 2004, 11:17:27 ; Search time 1154 Seconds  
(without alignments)  
11504.523 Million cell updates/sec

Title: US-10-624-932-1  
Perfect score: 2752  
Sequence: 1 ccgcggggcccgcgcccg.....tgagtgctgaggccgcccag 2752

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3163042 seqs, 2412103800 residues

Total number of hits satisfying chosen parameters: 6326084

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
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- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq2:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	% Query
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No.	Score	Match	Length	DB	ID	Description
1	2752	100.0	2752	13	US-09-918-779-1	Sequence 1, Appli
2	2752	100.0	2752	17	US-10-624-932-1	Sequence 1, Appli
3	2676.4	97.3	2881	11	US-09-970-944-1	Sequence 1, Appli
4	2356	85.6	3580	17	US-10-311-623-13	Sequence 13, Appl
5	2259	82.1	3014	10	US-09-933-261-1	Sequence 1, Appli
6	2259	82.1	3014	15	US-10-256-702-1	Sequence 1, Appli
7	2252.2	81.8	2697	15	US-10-240-154-15	Sequence 15, Appl
8	1562.4	56.8	1787	10	US-09-933-261-2	Sequence 2, Appli
9	1562.4	56.8	1787	15	US-10-256-702-2	Sequence 2, Appli
10	1206.6	43.8	1321	13	US-10-296-115-365	Sequence 365, App
11	1155.8	42.0	1282	9	US-09-833-381-1806	Sequence 1806, Ap
12	936.2	34.0	2860	13	US-10-087-684-1	Sequence 1, Appli
13	936.2	34.0	2860	13	US-10-087-684-3	Sequence 3, Appli
14	936.2	34.0	2860	13	US-10-218-779-1	Sequence 1, Appli
15	936.2	34.0	2860	13	US-10-218-779-3	Sequence 3, Appli
16	913.6	33.2	2895	13	US-10-037-417-37	Sequence 37, Appl
17	904	32.8	3485	9	US-09-816-828-18	Sequence 18, Appl
18	902.4	32.8	3884	13	US-10-147-493-145	Sequence 145, App
19	902.4	32.8	3884	13	US-10-145-127-145	Sequence 145, App
20	902.4	32.8	3884	13	US-10-160-503-145	Sequence 145, App
21	902.4	32.8	3884	13	US-10-143-118-145	Sequence 145, App
22	902.4	32.8	3884	13	US-10-144-993-145	Sequence 145, App
23	902.4	32.8	3884	13	US-10-158-787-145	Sequence 145, App
24	902.4	32.8	3884	13	US-10-140-024-145	Sequence 145, App
25	902.4	32.8	3884	13	US-10-140-808-145	Sequence 145, App
26	902.4	32.8	3884	13	US-10-152-405-145	Sequence 145, App
27	902.4	32.8	3884	13	US-10-127-852A-145	Sequence 145, App
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29	902.4	32.8	3884	13	US-10-128-685A-145	Sequence 145, App
30	902.4	32.8	3884	13	US-10-131-820A-145	Sequence 145, App
31	902.4	32.8	3884	13	US-10-142-886-145	Sequence 145, App
32	902.4	32.8	3884	13	US-10-146-728-145	Sequence 145, App
33	902.4	32.8	3884	13	US-10-146-786-145	Sequence 145, App
34	902.4	32.8	3884	13	US-10-147-499-145	Sequence 145, App
35	902.4	32.8	3884	13	US-10-157-798-145	Sequence 145, App
36	902.4	32.8	3884	15	US-10-028-072-145	Sequence 145, App
37	902.4	32.8	3884	15	US-10-121-049-145	Sequence 145, App
38	902.4	32.8	3884	15	US-10-123-904-145	Sequence 145, App
39	902.4	32.8	3884	15	US-10-140-470-145	Sequence 145, App
40	902.4	32.8	3884	15	US-10-175-746-145	Sequence 145, App
41	902.4	32.8	3884	15	US-10-176-918-145	Sequence 145, App
42	902.4	32.8	3884	15	US-10-176-921-145	Sequence 145, App
43	902.4	32.8	3884	15	US-10-137-865-145	Sequence 145, App
44	902.4	32.8	3884	15	US-10-140-474-145	Sequence 145, App
45	902.4	32.8	3884	15	US-10-142-431-145	Sequence 145, App

#### ALIGNMENTS

##### RESULT 1

US-09-918-779-1

; Sequence 1, Application US/09918779

; Publication No. US20030064369A1

; GENERAL INFORMATION:

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; APPLICANT: Taupier, Raymond
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/09/918,779
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,762
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,770
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,769
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/225,146
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,392
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,470
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,697
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/263,662
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/281,645
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2752
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-779-1

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Query Match          100.0%; Score 2752; DB 13; Length 2752;
Best Local Similarity 100.0%; Pred. No. 0;

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Matches 2752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CCGCGGGGCCCCGCGCCCGGCCCGCCCGCTGCCCCCGCGGCCATGGCCGTCCGGCCC 60
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Db      1 CCGCGGGGCCCCGCGCCCGGCCCGCCCGCTGCCCCCGCGGCCATGGCCGTCCGGCCC 60

Qy     61 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 120
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Qy    121 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 180
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Db    121 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 180

Qy    181 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240
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Qy    241 AAGGCCGTGCCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 300
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Db    241 AAGGCCGTGCCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 300

Qy    301 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCACCATGGAGGTCCGC 360
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Db    301 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCACCATGGAGGTCCGC 360

Qy    361 ATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTCTGGGCTGGAGGAATACTGGTGCCAG 420
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Db    361 ATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTCTGGGCTGGAGGAATACTGGTGCCAG 420

Qy    421 TGGCTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 480
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Db    421 TGGCTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 480

Qy    481 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 540
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Db    481 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 540

Qy    541 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600
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Db    541 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600

Qy    601 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 660
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 660

Qy    661 CTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC 720
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC 720

Qy    721 ATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTTCATCGTCTACGTGAACGGTGGGTGG 780
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTTCATCGTCTACGTGAACGGTGGGTGG 780

Qy    781 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG 840
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG 840
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Db	841	AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT	900
Qy	901	GTCCAGAAAACAGCCTGCGCCACCCTGTGCCAGTAGACGGCAGCTGGAGCCCGTGGAGC	960
Db	901	GTCCAGAAAACAGCCTGCGCCACCCTGTGCCAGTAGACGGCAGCTGGAGCCCGTGGAGC	960
Qy	961	AAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCA	1020
Db	961	AAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCA	1020
Qy	1021	GCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACC	1080
Db	1021	GCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACC	1080
Qy	1081	AGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTC	1140
Db	1081	AGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTC	1140
Qy	1141	ATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCATCCTCGTTTATTGCCGG	1200
Db	1141	ATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCATCCTCGTTTATTGCCGG	1200
Qy	1201	AAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTCCAG	1260
Db	1201	AAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTCCAG	1260
Qy	1261	CCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCGGAC	1320
Db	1261	CCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCGGAC	1320
Qy	1321	CTCAGCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCCAGC	1380
Db	1321	CTCAGCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCCAGC	1380
Qy	1381	CCCAAGTTCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACACA	1440
Db	1381	CCCAAGTTCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACACA	1440
Qy	1441	CTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAG	1500
Db	1441	CTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAG	1500
Qy	1501	AACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTC	1560
Db	1501	AACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTC	1560
Qy	1561	CTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCC	1620
Db	1561	CTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCC	1620
Qy	1621	ATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGG	1680
Db	1621	ATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGG	1680



Qy	1681	TTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCTGGC	1740
Db	1681	TTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCTGGC	1740
Qy	1741	GTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGAC	1800
Db	1741	GTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGAC	1800
Qy	1801	AGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCAC	1860
Db	1801	AGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCAC	1860
Qy	1861	CTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTAC	1920
Db	1861	CTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTAC	1920
Qy	1921	GTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCC	1980
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Qy	1981	GCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAAC	2040
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Qy	2041	ATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAG	2100
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Qy	2101	AAGCAGCTGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTCAAGGACAGTTAC	2160
Db	2101	AAGCAGCTGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTCAAGGACAGTTAC	2160
Qy	2161	CACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTT	2220
Db	2161	CACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTT	2220
Qy	2221	GTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCAC	2280
Db	2221	GTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCAC	2280
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Qy	2341	GTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAGGAC	2400
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Qy	2401	ACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGC	2460
Db	2401	ACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGC	2460
Qy	2461	CCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGACCCA	2520
Db	2461	CCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGACCCA	2520
Qy	2521	CCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAGCCAT	2580

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Qy      2581  CTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCG 2640
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Db      2581  CTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCG 2640
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Db      2641  CGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAG 2700
Qy      2701  CCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGAGGCCGGCCAG 2752
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RESULT 2

US-10-624-932-1

; Sequence 1, Application US/10624932

; Publication No. US20040096877A1

; GENERAL INFORMATION:

; APPLICANT: Taupier, Raymond

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Rastelli, Luca

; APPLICANT: Spaderna, Steven

; APPLICANT: Shimkets, Richard

; APPLICANT: Zerhusen, Bryan

; APPLICANT: Spytek, Kimberly

; APPLICANT: Shenoy, Suresh

; APPLICANT: Li, Li

; APPLICANT: Gusev, Vladimir

; APPLICANT: Grosse, William

; APPLICANT: Alsobrook, John

; APPLICANT: Lepley, Denise

; APPLICANT: Burgess, Catherine

; APPLICANT: Gerlach, Valerie

; APPLICANT: Ellerman, Karen

; APPLICANT: MacDougall, John

; APPLICANT: Stone, David

; APPLICANT: Smithson, Glennnda

; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-074 US

; CURRENT APPLICATION NUMBER: US/10/624,932

; CURRENT FILING DATE: 2003-07-21

; PRIOR APPLICATION NUMBER: 09/918,779

; PRIOR FILING DATE: 2001-07-03

; PRIOR APPLICATION NUMBER: 60/221,409

; PRIOR FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: 60/222,840

; PRIOR FILING DATE: 2000-08-04

; PRIOR APPLICATION NUMBER: 60/223,752

; PRIOR FILING DATE: 2000-08-08

; PRIOR APPLICATION NUMBER: 60/223,762

; PRIOR FILING DATE: 2000-08-08

; PRIOR APPLICATION NUMBER: 60/223,770

; PRIOR FILING DATE: 2000-08-08

; PRIOR APPLICATION NUMBER: 60/223,769

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; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/225,146
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,392
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,470
; PRIOR FILING DATE: 2000-08-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2752
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-624-932-1

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Query Match          100.0%; Score 2752; DB 17; Length 2752;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CCGCGGGGCCCCGCGCCCGGCCCGCCGCTGCCCCGCCGCGGCCATGGCCGTCCGGCCC 60
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Qy     61 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 120
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Qy    121 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 180
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Qy    181 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240
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Db    181 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240

Qy    241 AAGGCCGTGCCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 300
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Db    241 AAGGCCGTGCCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 300

Qy    301 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGC 360
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Qy    421 TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 480
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Qy    481 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 540
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Db	541	 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG	600
Qy	601	AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC	660
Db	601	 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC	660
Qy	661	CTGGTGGTGCGACAGGCCCCGCTTGCTGACACGGCCAACCTACACCTGCGTGGCCAAGAAC	720
Db	661	 CTGGTGGTGCGACAGGCCCCGCTTGCTGACACGGCCAACCTACACCTGCGTGGCCAAGAAC	720
Qy	721	ATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG	780
Db	721	 ATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG	780
Qy	781	TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG	840
Db	781	 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG	840
Qy	841	AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT	900
Db	841	 AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT	900
Qy	901	GTCCAGAAAACAGCCTGCGCCACCCTGTGCCAGTAGACGGCAGCTGGAGCCCGTGGAGC	960
Db	901	 GTCCAGAAAACAGCCTGCGCCACCCTGTGCCAGTAGACGGCAGCTGGAGCCCGTGGAGC	960
Qy	961	AAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCA	1020
Db	961	 AAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCA	1020
Qy	1021	GCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACC	1080
Db	1021	 GCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACC	1080
Qy	1081	AGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTC	1140
Db	1081	 AGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTC	1140
Qy	1141	ATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCATCCTCGTTTATTGCCGG	1200
Db	1141	 ATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCATCCTCGTTTATTGCCGG	1200
Qy	1201	AAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTCCAG	1260
Db	1201	 AAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTCCAG	1260
Qy	1261	CCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCGGAC	1320
Db	1261	 CCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCGGAC	1320
Qy	1321	CTCAGCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCCAGC	1380
Db	1321	 CTCAGCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCCAGC	1380
Qy	1381	CCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACACA	1440

Db	1381	CCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACACA	1440
Qy	1441	CTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAG	1500
Db	1441	CTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAG	1500
Qy	1501	AACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTC	1560
Db	1501	AACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTC	1560
Qy	1561	CTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCC	1620
Db	1561	CTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGATGCC	1620
Qy	1621	ATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGG	1680
Db	1621	ATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGG	1680
Qy	1681	TTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCTGGC	1740
Db	1681	TTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCTGGC	1740
Qy	1741	GTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGAC	1800
Db	1741	GTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGAC	1800
Qy	1801	AGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCAC	1860
Db	1801	AGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCAC	1860
Qy	1861	CTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTAC	1920
Db	1861	CTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTAC	1920
Qy	1921	GTCTTCACCGAGCAGCTGGGCGCCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCC	1980
Db	1921	GTCTTCACCGAGCAGCTGGGCGCCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCC	1980
Qy	1981	GCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAAC	2040
Db	1981	GCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAAC	2040
Qy	2041	ATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAG	2100
Db	2041	ATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAG	2100
Qy	2101	AAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTCAAGGACAGTTAC	2160
Db	2101	AAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTCAAGGACAGTTAC	2160
Qy	2161	CACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGGAAGAGTAAGCTCCTT	2220
Db	2161	CACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGGAAGAGTAAGCTCCTT	2220
Qy	2221	GTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCAC	2280
Db	2221	GTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCAC	2280

Qy 2281 TGCACCTTCACCTGGAGCGTGTCTAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGG 2340  
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 Db 2281 TGCACCTTCACCTGGAGCGTGTCTAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGG 2340  
 Qy 2341 GTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAGGAC 2400  
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 Db 2341 GTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAGGAC 2400  
 Qy 2401 ACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGTCCCAGCCCTGGTGGGC 2460  
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 Db 2401 ACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGTCCCAGCCCTGGTGGGC 2460  
 Qy 2461 CCCAGTGCCTTCAAGATCCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGACCCA 2520  
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 Db 2461 CCCAGTGCCTTCAAGATCCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGACCCA 2520  
 Qy 2521 CCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAGCCAT 2580  
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 Db 2521 CCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAGCCAT 2580  
 Qy 2581 CTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCG 2640  
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 Db 2581 CTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCG 2640  
 Qy 2641 CGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAG 2700  
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 Db 2641 CGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAG 2700  
 Qy 2701 CCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGAGGCCGGCCAG 2752  
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 Db 2701 CCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGAGGCCGGCCAG 2752

RESULT 3

US-09-970-944-1

; Sequence 1, Application US/09970944

; Publication No. US20030204052A1

; GENERAL INFORMATION:

; APPLICANT: Herrman, John L

; APPLICANT: Rastelli, Luca

; APPLICANT: Shimkets, Richard A

; TITLE OF INVENTION: No. US20030204052A1e1 Proteins and Nucleic Acids Encoding Same and

; TITLE OF INVENTION: Antibodies Directed Against these Proteins

; FILE REFERENCE: 21402-138

; CURRENT APPLICATION NUMBER: US/09/970,944

; CURRENT FILING DATE: 2002-05-02

; PRIOR APPLICATION NUMBER: 60/237,862

; PRIOR FILING DATE: 2000-10-04

; NUMBER OF SEQ ID NOS: 62

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 2881

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-970-944-1

Query Match 97.3%; Score 2676.4; DB 11; Length 2881;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 2728; Conservative 0; Mismatches 21; Indels 9; Gaps 3;

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Qy      1 CCGCGGGGCCCCGCGCCCGGCCCGCCCGCCTGCCCGCCCGCGGCCATGGCCGTCCGGCCC 60
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Db     42 CCGCGGGGCCCCGCGCCCGGCCCGCCCGCCTGCCCGCCCGCGGCCATGGCCGTCCGGCCC 101

Qy     61 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 120
      |||
Db    102 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 161

Qy    121 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 180
      |||
Db    162 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 221

Qy    181 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240
      |||
Db    222 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 281

Qy    241 AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 300
      |||
Db    282 AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 341

Qy    301 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGC 360
      |||
Db    342 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGTGGAGCCGACCATGGAGGTCCGC 401

Qy    361 ATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCTGGGCTGGAGGAATACTGGTGCCAG 420
      |||
Db    402 ATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCTGGGCTGGAGGAATACTGGTGCCAG 461

Qy    421 TGCCTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 480
      |||
Db    462 TGCCTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 521

Qy    481 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 540
      |||
Db    522 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 581

Qy    541 ATCGTGCTGCCCTGCCGTCCACCGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600
      |||
Db    582 ATCGTGCTGCCCTGCCGTCCACCGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 641

Qy    601 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 660
      |||
Db    642 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 701

Qy    661 CTGGTGGTGGCAGAGGCCCGCCTTGCTGACACGGCCAACCTACACCTGCGTGGCCAAGAAC 720
      |||
Db    702 CTGGTGGTGGCAGAGGCCCGCCTTGCTGACACGGCCAACCTACACCTGCGTGGCCAAGAAC 761

Qy    721 ATCGTGGCACGTGCGCGCAGCGCCTCCGCTGCTGTATCGTCTACGTGAACGGTGGGTGG 780
      |||
Db    762 ATCGTGGCACGTGCGCGCAGCGCCTCCGCTGCTGTATCGTCTACGTGAACGGTGGGTGG 821
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Qy	781	TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG	840
Db	822	TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG	881
Qy	841	AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT	900
Db	882	AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT	941
Qy	901	GTCCAGAA---AACAGCCTGCGCCACCCTGTGCCAGTAGACGGCAGCTGGAGCCCGTGG	957
Db	942	GTCCATGACCGCACCGTCTCCTCTCTGCTTGTCTCTGTGGACGGCAGCTGGAGCCCGTGG	1001
Qy	958	AGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGAC	1017
Db	1002	AGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGAC	1061
Qy	1018	CCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGT	1077
Db	1062	CCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGT	1121
Qy	1078	ACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGC	1137
Db	1122	ACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGC	1181
Qy	1138	CTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCCTCATCCTCGTTTATTGC	1197
Db	1182	CTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCCTCATCCTCGTTTATTGC	1241
Qy	1198	CGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTC	1257
Db	1242	CGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTC	1301
Qy	1258	CAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCG	1317
Db	1302	CAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCG	1361
Qy	1318	GACCTCAGCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCC	1377
Db	1362	GACCTCAG---CACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCC	1418
Qy	1378	AGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCAC	1437
Db	1419	AGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCAC	1478
Qy	1438	ACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCTCTCCACC	1497
Db	1479	ACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCTCTCCACC	1538
Qy	1498	CAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAAC	1557
Db	1539	CAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAAC	1598
Qy	1558	TTCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGAT	1617
Db	1599	TTCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCAGAT	1658
Qy	1618	GCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTG	1677



Db	1659	 GCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTG	1718
Qy	1678	AGGTTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCCT	1737
Db	1719	 AGGTTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCCT	1778
Qy	1738	GGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCT	1797
Db	1779	 GGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCT	1838
Qy	1798	GACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGG---AGGATGTG	1854
Db	1839	 GACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGCAGGATGTG	1898
Qy	1855	CTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCC	1914
Db	1899	 CTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCC	1958
Qy	1915	TGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTG	1974
Db	1959	 TGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTG	2018
Qy	1975	GCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAG	2034
Db	2019	 GCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAG	2078
Qy	2035	TACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAG	2094
Db	2079	 TACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAG	2138
Qy	2095	CTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGAC	2154
Db	2139	 CTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGAC	2198
Qy	2155	AGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAG	2214
Db	2199	 AGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAG	2258
Qy	2215	CTCCTTGTCAGCTACCAGGAGATCCCC'TTTTATCACATCTGGAATGGCACGCAGCGGTAC	2274
Db	2259	 CTCCTTGTCAGCTACCAGGAGATCCCC'TTTTATCACATCTGGAATGGCACGCAGCGGTAC	2318
Qy	2275	TTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAG	2334
Db	2319	 TTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAG	2378
Qy	2335	CTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACC	2394
Db	2379	 CTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACC	2438
Qy	2395	AAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTG	2454
Db	2439	 AAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTG	2498
Qy	2455	GTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTG	2514

Db 2499 GTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTG 2558  
 Qy 2515 GACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGAC 2574  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2559 GACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGAC 2618  
 Qy 2575 AGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGG 2634  
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 Db 2619 AGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGG 2678  
 Qy 2635 GAGGCGCGGCACCTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTG 2694  
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 Db 2679 GAGGCGCGGCACCTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTG 2738  
 Qy 2695 GGCCAGCCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGAGGCCGGCCAG 2752  
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 Db 2739 GGCCAGCCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGAGGCCGGCCAG 2796

RESULT 4

US-10-311-623-13

; Sequence 13, Application US/10311623

; Publication No. US20040023244A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.; GRIFFIN, Jennifer A.

; APPLICANT: KALLICK, Deborah A.; TRIBOULEY, Catherine M.

; APPLICANT: YUE, Henry; NGUYEN, Dannel B.

; APPLICANT: TANG, Y. Tom; LAL, Preeti G.

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; APPLICANT: LU, Dyung Aina M.; GRAUL, Richard C.

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; APPLICANT: HAFALIA, April J. A.; BAUGHN, Mariah R.

; APPLICANT: BANDMAN, Olga; ARVIZU, Chandra S.

; APPLICANT: YANG, Junming; XU, Yuming

; APPLICANT: GANDHI, Ameena R.; WARREN, Bridget A.

; APPLICANT: DING, Li; SANJANWALA, Madhusudan M.

; APPLICANT: DUGGAN, Brendan M.; LU, Yan

; TITLE OF INVENTION: RECEPTORS

; FILE REFERENCE: PF-0793 USN

; CURRENT APPLICATION NUMBER: US/10/311,623

; CURRENT FILING DATE: 2002-12-17

; PRIOR APPLICATION NUMBER: US 01/19942

; PRIOR FILING DATE: 2001-06-21

; PRIOR APPLICATION NUMBER: US 60/214,027

; PRIOR FILING DATE: 2000-06-21

; PRIOR APPLICATION NUMBER: US 60/228,045

; PRIOR FILING DATE: 2000-08-25

; PRIOR APPLICATION NUMBER: US 60/255,104

; PRIOR FILING DATE: 2000-12-12

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PERL Program

; SEQ ID NO 13

; LENGTH: 3580

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; OTHER INFORMATION: Incyte ID No. US20040023244A1 6052371CB1  
US-10-311-623-13

Query Match 85.6%; Score 2356; DB 17; Length 3580;  
Best Local Similarity 93.6%; Pred. No. 0;  
Matches 2537; Conservative 0; Mismatches 5; Indels 168; Gaps 1;

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Qy     103 CTCCGCGGCTCGGGTGCCAGCAGAGTGCCACCGTGCCCAACCCAGTGCCTGGTGCCAAC 162
      |||||||
Db     61  CTCCGCGGCTCGGGTGCCAGCAGAGTGCCACCGTGCCCAACCCAGTGCCTGGTGCCAAC 120

Qy     163 CCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAG 222
      |||||||
Db    121  CCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAG 180

Qy     223 CCAGTGCTGCTTGTGTGCAAGGCCGTGCCC GCCACGCAGATCTTCTTCAAGTGCAACGGG 282
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Db    181  CCAGTGCTGCTTGTGTGCAAGGCCGTGCCC GCCACGCAGATCTTCTTCAAGTGCAACGGG 240

Qy     283 GAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTG 342
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Db    241  GAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTG 300

Qy     343 CCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTCCGGGCTG 402
      |||||||
Db    301  CCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTCCGGGCTG 360

Qy     403 GAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAG 462
      |||||||
Db    361  GAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAG 420

Qy     463 GCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAG 522
      |||||||
Db    421  GCCTACATCCGCATAGCCTATTTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAG 480

Qy     523 GTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGAGGGGCATCCCTCCAGCC 582
      |||||||
Db    481  GTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGAGGGGCATCCCTCCAGCC 540

Qy     583 GAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATAC 642
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Db    541  GAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATAC 600

Qy     643 ATCACGCGGGAGCACAGCCTGGTGGTGCACAGGCCCGCCTTGCTGACACGGCCAACCTAC 702
      |||||||
Db    601  ATCACGCGGGAGCACAGCCTGGTGGTGCACAGGCCCGCCTTGCTGACACGGCCAACCTAC 660

Qy     703 ACCTGCGTGGCCAAGAACATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTATCGTC 762
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Db    661  ACCTGCGTGGCCAAGAACATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTATCGTC 720

Qy     763 TACGTGAACGGTGGGTGGTGCACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGG 822
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Db	721	TACGTG-----	726
Qy	823	CGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCT	882
Db	727	-----	726
Qy	883	TTCTGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGC	942
Db	727	-----GACGGC	732
Qy	943	AGCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGC	1002
Db	733	AGCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGC	792
Qy	1003	CGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTG	1062
Db	793	CGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTG	852
Qy	1063	GACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTG	1122
Db	853	GACACCCGCAACTGTACCAGTGACCTCTGTGTACACACTGCTTCTGGCCCTGAGGACGTG	912
Qy	1123	GCCCTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTC	1182
Db	913	GCCCTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTC	972
Qy	1183	ATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATT	1242
Db	973	ATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATT	1032
Qy	1243	CTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTG	1302
Db	1033	CTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTG	1092
Qy	1303	CTCACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCC	1362
Db	1093	CTCACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCC	1152
Qy	1363	CGGCAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTG	1422
Db	1153	CGGCAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTG	1212
Qy	1423	GGTGGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTC	1482
Db	1213	GGTGGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTC	1272
Qy	1483	TCCCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACC	1542
Db	1273	TCCCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACC	1332
Qy	1543	TATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTC	1602
Db	1333	TATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGAATCAGCCTC	1392
Qy	1603	CTCATCCCCCAGATGCCATAACCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCAC	1662
Db	1393	CTCATCCCCCAGATGCCATAACCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCAC	1452

Qy	1663	AAGCCGGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTT	1722
Db	1453	AAGCCGGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTT	1512
Qy	1723	AGCTGTGGACCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGT	1782
Db	1513	AGCTGTGGACCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGT	1572
Qy	1783	GGGGAGCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGC	1842
Db	1573	GGGGAGCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGC	1632
Qy	1843	TGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTG	1902
Db	1633	TGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTG	1692
Qy	1903	GAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAG	1962
Db	1693	GAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAG	1752
Qy	1963	GCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGC	2022
Db	1753	GCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGC	1812
Qy	2023	ACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAG	2082
Db	1813	ACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAG	1872
Qy	2083	GAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTG	2142
Db	1873	GAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTG	1932
Qy	2143	CACTTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTG	2202
Db	1933	CACTTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTG	1992
Qy	2203	TGGAAGAGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGC	2262
Db	1993	TGGAAGAGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGC	2052
Qy	2263	ACGCAGCGGTACTTGCACTGCACCTTCACCTGGAGCGTGTGAGCCCCAGCACTAGTGAC	2322
Db	2053	ACGCAGCGGTACTTGCACTGCACCTTCACCTGGAGCGTGTGAGCCCCAGCACTAGTGAC	2112
Qy	2323	CTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAAC	2382
Db	2113	CTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAAC	2172
Qy	2383	TTCAACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGG	2442
Db	2173	TTCAACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGG	2232
Qy	2443	GTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATA	2502
Db	2233	GTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATA	2292

Qy 2503 ATTTCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAA 2562  
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 Db 2293 ATTTCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAA 2352  
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 Db 2353 CTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATC 2412  
 Qy 2623 CTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCA 2682  
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 Db 2413 CTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCA 2472  
 Qy 2683 GTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGA 2742  
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 Db 2473 GTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGA 2532  
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 Db 2533 GGCCGGCCAG 2542

RESULT 5

US-09-933-261-1

; Sequence 1, Application US/09933261

; Publication No. US20030040046A1

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; Leonardo, E. David

; Hink, Lindsay

; Masu, Masayuki

; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 8

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; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/933,261

; FILING DATE: 20-Aug-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/808,982

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: OSMAN, RICHARD A

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: UC96-217

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; TELEPHONE: (415) 343-4341  
; TELEFAX: (415) 343-4342  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3014 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-933-261-1

Query Match 82.1%; Score 2259; DB 10; Length 3014;  
Best Local Similarity 89.7%; Pred. No. 0;  
Matches 2427; Conservative 0; Mismatches 280; Indels 0; Gaps 0;

Qy	46	ATGGCCGTCCGGCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGGCTC	105
Db	1	ATGGCCGTCCGGCCCGGCCTGTGGCCAGTGCCTGGGCATAGTCCTCGCCGCTTGGGCTT	60
Qy	106	CGCGGCTCGGGTGCCCAGCAGAGTGCCACCGTGCCCAACCCAGTGCCTGGTGCCAACCCG	165
Db	61	CGTGTTTCGGGTGCCAGCAGAGTGCCACGGTGCCCAATCCAGTGCCCGGTGCCAACCCC	120
Qy	166	GACCTGCTTCCCCACTTCCTGGTGGAGCCCAGGATGTGTACATCGTCAAGAACAAGCCA	225
Db	121	GACCTGCTGCCCCACTTCCTGGTAGAGCCTGAGGACGTGTACATTGTCAAGAACAAGCCG	180
Qy	226	GTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAG	285
Db	181	GTGTTGTTGGTGTGCAAGGCTGTGCCTGCCACCCAGATCTTCTTCAAGTGCAATGGGGAA	240
Qy	286	TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCC	345
Db	241	TGGGTCCGCCAGGTCGATCACGTAATTGAACGCAGCACCGACAGCAGCAGCGGATTGCCA	300
Qy	346	ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTCCGGCTGGAG	405
Db	301	ACCATGGAGGTCCGTATCAACGTATCGAGGCAGCAGGTAGAGAAAGTGTTTGGGCTGGAG	360
Qy	406	GAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC	465
Db	361	GAATACTGGTGCCAGTGTGTGGCATGGAGCTCCTCGGGTACCACCAAAAGTCAGAAGGCC	420
Qy	466	TACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG	525
Db	421	TACATCCGATTGCCTATTTGCGCAAGAACTTTGAGCAGGAGCCACTGGCCAAGGAAGTG	480
Qy	526	TCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAG	585
Db	481	TCACTGGAGCAAGGCATTGTACTACCTTGTGCCCCCAGAAGGAATCCCCCAGCTGAG	540
Qy	586	GTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATC	645
Db	541	GTGGAGTGGCTTCGAAATGAGGACCTCGTGGACCCCTCCCTCGATCCCAATGTGTACATC	600
Qy	646	ACGCGGGAGCACAGCCTGGTGGTGGCGACAGGCCCGCTTGCTGACACGGCCAACCTACACC	705

Db	601	ACGCGGGAGCACAGCCTAGTCGTGCGTCAGGCCCGCCTGGCCGACACGGCCAACTACACC	660
Qy	706	TGCGTGGCCAAGAACATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTCTAC	765
Db	661	TGTGTGGCCAAGAACATCGTAGCCCGTCGCCGAAGCACCTCTGCAGCGGTCAATTGTTTAT	720
Qy	766	GTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGC	825
Db	721	GTGAACGGTGGGTGGTTCGACGTGGACTGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGT	780
Qy	826	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTC	885
Db	781	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCACCTCTCAACGGGGGCGCCTTC	840
Qy	886	TGTGAGGGGCGAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGC	945
Db	841	TGTGAGGGGCGAGAATGTCCAGAAAACAGCCTGCGCCACTCTGTGCCCAGTGGATGGGAGC	900
Qy	946	TGGAGCCCGTGGAGCAAGTGGTGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGT	1005
Db	901	TGGAGTTCGTGGAGTAAGTGGTCAGCCTGTGGGCTTGACTGCACCCACTGGCGGAGCCGC	960
Qy	1006	GAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGAC	1065
Db	961	GAGTGCTCTGACCCAGCACCCCGCAATGGAGGTGAGGAGTGTGCGGGTGCTGACCTGGAC	1020
Qy	1066	ACCCGCAACTGTACCAAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCC	1125
Db	1021	ACCCGCAACTGTACCAAGTGACCTCTGCCTGCACACCGCTTCTTGCCCCGAGGACGTGGCT	1080
Qy	1126	CTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCTCTGCTGCTGCTTGTCTCATC	1185
Db	1081	CTCTACATCGGCCCTTGTGCTGTGGCTGTGTGCCTCTTCTTGCTGTTGTGCCCCCTTGA	1140
Qy	1186	CTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTC	1245
Db	1141	CTCATTTACTGTGCGAAGAAGGAAGGGCTGGACTCCGATGTGGCCGACTCGTCCATCCTC	1200
Qy	1246	ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTC	1305
Db	1201	ACCTCGGGCTTCCAGCCTGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCACCTGCTC	1260
Qy	1306	ACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG	1365
Db	1261	ACCATCCAGCCAGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTATGTTGAGG	1320
Qy	1366	CAGGATGGGCCCAGCCCCAAGTTCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGT	1425
Db	1321	CAGGATGGACCCAGCCCCAAGTTCAGCTCTCTAATGGTCACCTGCTCAGCCCCACTGGGG	1380
Qy	1426	GGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCC	1485
Db	1381	AGTGGCCGCCATACGTTGCACCACAGCTCACCCACCTCTGAGGCTGAGGACTTCGTCTCC	1440
Qy	1486	CGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTAT	1545



Db	1441	CGCCTCTCCACCCAAAACACTACTTTTCGTTCCCTGCCCGCGGCACCAACATGGCCTAC	1500
Qy	1546	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTC	1605
Db	1501	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACGGGGATCAGCCTCCTC	1560
Qy	1606	ATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG	1665
Db	1561	ATACCCCGGATGCCATCCCCGAGGAAAGATCTACGAGATCTACCTCACACTGCACAAG	1620
Qy	1666	CCGGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGC	1725
Db	1621	CCAGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCAGTCGTTAGC	1680
Qy	1726	TGTGGACCCCTGGCGTCTGCTCACCCGCCAGTCATCCTGGCTATGGACCACTGTGGG	1785
Db	1681	TGTGGGCCCCCAGGAGTCCTGCTCACCCGCCAGTCATCCTTGAATGGACCACTGTGGA	1740
Qy	1786	GAGCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG	1845
Db	1741	GAGCCAGCCCTGACAGCTGGAGTCTGCGCCTCAAAAAGCAGTCCTGCGAGGGCAGTTGG	1800
Qy	1846	GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAG	1905
Db	1801	GAGGATGTGCTGCACCTTGGTGAGGAGTCACCTTCCACCTCTACTACTGCCAGCTGGAG	1860
Qy	1906	GCCAGTGCCTGCTACGTCTTACCGAGCAGCTGGGCGCCTTTGCCCTGGTGGGAGAGGCC	1965
Db	1861	GCCGGGCGCTGCTATGTCTTACGGAGCAGCTGGGCGCCTTTGCCCTGGTAGGAGAGGCC	1920
Qy	1966	CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC	2025
Db	1921	CTCAGCGTGGCTGCCACCAAGCGCCTCAGGCTCCTTCTGTTTGCTCCCGTGGCCTGTACG	1980
Qy	2026	TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG	2085
Db	1981	TCCCTTGAGTACAACATCCGAGTGTACTGCCTACACGACACCCACGACGCTCTCAAGGAG	2040
Qy	2086	GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCAC	2145
Db	2041	GTGGTGCAGCTGGAGAAGCAGCTAGGTGGACAGCTGATCCAGGAGCCTCGCGTCTGCAC	2100
Qy	2146	TTCAAAGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGG	2205
Db	2101	TTCAAAGACAGTTACCACAACCTACGTCTCTCCATCCACGACGTGCCAGCTCCCTGTGG	2160
Qy	2206	AAGAGTAAGCTCCTTGTGAGCTACCAGGAGATCCCTTTTATCACATCTGGAATGGCACG	2265
Db	2161	AAGAGCAAGCTACTTGTGAGCTACCAGGAGATCCCTTTTACCACATCTGGAACGGCACC	2220
Qy	2266	CAGCGGTACTTGCACTGCACCTTACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTG	2325
Db	2221	CAGCAGTATCTGCACTGCACCTTACCCTGGAGCGCATCAACGCCAGCACCAGCGACCTG	2280
Qy	2326	GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTC	2385
Db	2281	GCCTGCAAGGTGTGGGTGTGGCAGGTGGAGGGGAGATGGGCAGAGCTTCAACATCAACTTC	2340



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;          CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: US/09/933,261
;          FILING DATE: 20-Aug-2001
;          APPLICATION NUMBER: 08/808,982
;          FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
;          NAME: OSMAN, RICHARD A
;          REGISTRATION NUMBER: 36,627
;          REFERENCE/DOCKET NUMBER: UC96-217
;
; TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (415) 343-4341
;          TELEFAX: (415) 343-4342
;
; INFORMATION FOR SEQ ID NO: 1:
;          SEQUENCE CHARACTERISTICS:
;              LENGTH: 3014 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: double
;              TOPOLOGY: linear
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;          MOLECULE TYPE: cDNA
;          SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-256-702-1

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Query Match          82.1%;   Score 2259;   DB 15;   Length 3014;
Best Local Similarity 89.7%;   Pred. No. 0;
Matches 2427;   Conservative    0;   Mismatches 280;   Indels    0;   Gaps    0;

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Db      1 ATGGCCGTCCGGCCCGGCCTGTGGCCAGTGTCTCCTGGGCATAGTCCTCGCCGCTTGGCTT 60

Qy     106 CGCGGCTCGGGTGCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCG 165
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Db      61 CGTGTTTCGGGTGCCAGCAGAGTGCCACGGTGGCCAATCCAGTGCCCGGTGCCAACCCC 120

Qy     166 GACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCA 225
          |||||||| |||||||||||||| |||| |||| ||||||||||||||||
Db     121 GACCTGCTGCCCCACTTCCTGGTAGAGCCTGAGGACGTGTACATTGTCAAGAACAAGCCG 180

Qy     226 GTGCTGCTTGTGTGCAAGGCCGTGCCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAG 285
          ||| || | |||||||||| |||| |||| |||||||||||||||||| ||||
Db     181 GTGTTGTTGGTGTGCAAGGCTGTGCCTGCCACCCAGATCTTCTTCAAGTGCAATGGGGAA 240

Qy     286 TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCC 345
          |||| |||||||| || |||| || || |||||||| || | |||| || ||||
Db     241 TGGGTCCGCCAGGTCGATCACGTAATTGAACGCAGCACCGACAGCAGCAGCGGATTGCCA 300

Qy     346 ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTGCGAGAAGGTGTTTCGGGCTGGAG 405
          |||||||||||||| || || || || |||||||||| |||| |||| ||||||||
Db     301 ACCATGGAGGTCCGTATCAACGTATCGAGGCAGCAGGTAGAGAAAGTGTTTGGGCTGGAG 360

Qy     406 GAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC 465
          |||||||||||||| |||||||||||||| |||||||||| |||||||||| ||||
Db     361 GAATACTGGTGCCAGTGTGTGGCATGGAGCTCCTCGGGTACCACCAAAAGTCAGAAGGCC 420

Qy     466 TACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG 525
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Db	421	TACATCCGGATTGCCTATTTGCGCAAGAACTTTTGACGAGGAGCCACTGGCCAAGGAAGTG	480
Qy	526	TCCCTGGAGCAGGGCATCGTGTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAG 	585
Db	481	TCACTGGAGCAAGGCATTGTACTACCTTGTGCCCCCCCAGAAGGAATCCCCCAGCTGAG	540
Qy	586	GTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATC 	645
Db	541	GTGGAGTGGCTTCGAAATGAGGACCTCGTGGACCCCTCCCTCGATCCCAATGTGTACATC	600
Qy	646	ACGCGGGAGCACAGCCTGGTGGTGCACAGGCCCGCCTTGCTGACACGGCCAAC TACACC 	705
Db	601	ACGCGGGAGCACAGCCTAGTCGTGCGTCAGGCCCGCCTGGCCGACACGGCCAAC TACACC	660
Qy	706	TGCGTGGCCAAGAACATCGTGGCACGTGCGCCGAGCGCCTCCGCTGCTGTCATCGTCTAC 	765
Db	661	TGTGTGGCCAAGAACATCGTAGCCCGTCGCCGAAGCACCTCTGCAGCGGT CATTGTTTAT	720
Qy	766	GTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGC 	825
Db	721	GTGAACGGTGGGTGGTTCGACGTGGACTGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGT	780
Qy	826	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTC 	885
Db	781	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCACCTCTCAACGGGGGCGCCTTC	840
Qy	886	TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCAGTAGACGGCAGC 	945
Db	841	TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACTCTGTGCCAGTGGATGGGAGC	900
Qy	946	TGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGT 	1005
Db	901	TGGAGTTCGTGGAGTAAGTGGTCAGCCTGTGGGCTTGACTGCACCCACTGGCGGAGCCGC	960
Qy	1006	GAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGAC 	1065
Db	961	GAGTGCTCTGACCCAGCACCCCGCAATGGAGGTGAGGAGTGTGCGGGTGCTGACCTGGAC	1020
Qy	1066	ACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCC 	1125
Db	1021	ACCCGCAACTGTACCAGTGACCTCTGCCTGCACACCGCTTCTTGCCCCGAGGACGTGGCT	1080
Qy	1126	CTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCTCATC 	1185
Db	1081	CTCTACATCGGCCTTGTGCGTGTGGCTGTGTGCCTCTTCTTGCTGTTGCTGGCCCTTGA	1140
Qy	1186	CTCGTTTTATTGCCGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTC 	1245
Db	1141	CTCATTTACTGTCGCAAGAAGGAAGGGCTGGACTCCGATGTGGCCGACTCGTCCATCCTC	1200
Qy	1246	ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTC 	1305
Db	1201	ACCTCGGGCTTCCAGCCTGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCACCTGCTC	1260
Qy	1306	ACCATCCAGCCGGACCTCAGCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG 	1365
Db	1261	ACCATCCAGCCAGACCTCAGCACCACC ACTACCACCTACCAGGGCAGTCTATGTTTCGAGG	1320

Qy	1366	CAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGT	1425
Db	1321	CAGGATGGACCCAGCCCCAAGTTCCAGCTCTCTAATGGTCACCTGCTCAGCCCACTGGGG	1380
Qy	1426	GGCGGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCC	1485
Db	1381	AGTGGCCGCCATACGTTGCACCACAGCTCACCCACCTCTGAGGCTGAGGACTTCGTCTCC	1440
Qy	1486	CGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTAT	1545
Db	1441	CGCCTCTCCACCCAAAATACTTTTCGTTCCCTGCCCCGCGGCACCAGCAACATGGCCTAC	1500
Qy	1546	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTC	1605
Db	1501	GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACGGGGATCAGCCTCCTC	1560
Qy	1606	ATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG	1665
Db	1561	ATACCCCGGATGCCATCCCCCGAGGAAAGATCTACGAGATCTACCTCACACTGCACAAG	1620
Qy	1666	CCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGC	1725
Db	1621	CCAGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCAGTCGTTAGC	1680
Qy	1726	TGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGG	1785
Db	1681	TGTGGGCCCCCAGGAGTCCTGCTCACCCGGCCAGTCATCCTTGCAATGGACCACTGTGGA	1740
Qy	1786	GAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG	1845
Db	1741	GAGCCCAGCCCTGACAGCTGGAGTCTGCGCCTCAAAAAGCAGTCCTGCGAGGGCAGTTGG	1800
Qy	1846	GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAG	1905
Db	1801	GAGGATGTGCTGCACCTTGGTGAGGAGTCACCTTCCCACCTCTACTACTGCCAGCTGGAG	1860
Qy	1906	GCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCC	1965
Db	1861	GCCGGGGCCTGCTATGTCTTCACGGAGCAGCTGGGCCGCTTTGCCCTGGTAGGAGAGGCC	1920
Qy	1966	CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC	2025
Db	1921	CTCAGCGTGGCTGCCACCAAGCGCCTCAGGCTCCTTCTGTTTGCTCCCGTGGCCTGTACG	1980
Qy	2026	TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG	2085
Db	1981	TCCCTTGAGTACAACATCCGAGTGTACTGCCTACACGACACCCACGACGCTCTCAAGGAG	2040
Qy	2086	GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCAC	2145
Db	2041	GTGGTGCAGCTGGAGAAGCAGCTAGGTGGACAGCTGATCCAGGAGCCTCGCGTCTGCAC	2100
Qy	2146	TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGG	2205
Db	2101	TTCAAAGACAGTTACCACAACCTACGTCTCTCCATCCACGACGTGCCAGCTCCCTGTGG	2160

Qy	2206	AAGAGTAAGCTCCTTGT	CAGCTACCAGGAGATCCCTTTTATCACATCTGGAATGGCACG	2265	
Db	2161	AAGAGCAAGCTACTTGT	CAGCTACCAGGAGATCCCTTTTACCACATCTGGAACGGCACC	2220	
Qy	2266	CAGCGGTACTTGC	ACTGCACCTTACCCTGGAGCGTGT	CAGCCCCAGCACTAGTGACCTG	2325
Db	2221	CAGCAGTATCTGC	ACTGCACCTTACCCTGGAGCGCATCAACGCCAGCACCAGCGACCTG	2280	
Qy	2326	GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTC	2385		
Db	2281	GCCTGCAAGGTGTGGGTGTGGCAGGTGGAGGGAGATGGGCAGAGCTTCAACATCAACTTC	2340		
Qy	2386	AACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTTC	2445		
Db	2341	AACATCACTAAGGACACAAGGTTTGCTGAATTGTTGGCTCTGGAGAGTGAAGGGGGGGTTC	2400		
Qy	2446	CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATT	2505		
Db	2401	CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAAAAGATCATC	2460		
Qy	2506	TCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTC	2565		
Db	2461	GCCAGTCTGGACCCACCCTGCAGCCGGGGCGCCGACTGGAGAACTCTAGCCCAGAACTT	2520		
Qy	2566	CACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTC	2625		
Db	2521	CACCTGGACAGCCATCTTAGCTTCTTTGCCTCCAAGCCCAGCCCTACAGCCATGATCCTC	2580		
Qy	2626	AACCTGTGGGAGGCGCGGCACCTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTG	2685		
Db	2581	AACCTATGGGAGGCACGGCACCTTCCCCAACGGCAACCTCGGCCAGCTGGCAGCAGCTGTG	2640		
Qy	2686	GCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGCTGAGGC	2745		
Db	2641	GCCGGACTGGGCCAACCAGATGCTGGCCTCTTCACGGTGTCTGGAGGCCGAGTGTTGAGAC	2700		
Qy	2746	CGGCCAG	2752		
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US-10-240-154-15

; Publication No. US20030175741A1

; APPLICANT: Cochran et al.

; FILE REFERENCE: CKFW-P01-006

; CURRENT FILING DATE: 2001-04-02

; PRIOR FILING DATE: 2001-04-02

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; SOFTWARE: PatentIn version 3.2
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; LENGTH: 2697

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; TYPE: DNA
; ORGANISM: Rattus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2697)
US-10-240-154-15
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Query Match 81.8%; Score 2252.2; DB 15; Length 2697;  
Best Local Similarity 89.7%; Pred. No. 0;  
Matches 2419; Conservative 0; Mismatches 278; Indels 0; Gaps 0;

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Qy	106	CGCGGCTCGGGTGCCAGCAGAGTGCCACCGTGGCCAACCAGTGCCCTGGTGCCAACCCG	165
Db	61	CGTGTTTCGGGTGCCAGCAGAGTGCCACGGTGCCAATCCAGTGCCCGGTGCCAACCCC	120
Qy	166	GACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCA	225
Db	121	GACCTGCTGCCCCACTTCCTGGTAGAGCCTGAGGACGTGTACATTGTCAAGAACAAGCCG	180
Qy	226	GTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAG	285
Db	181	GTGTTGTTGGTGTGCAAGGCTGTGCCTGCCACCCAGATCTTCTTCAAGTGCAATGGGGAA	240
Qy	286	TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCC	345
Db	241	TGGGTCCGCCAGGTCGATCACGTAATTGAACGCAGCACCGACAGCAGCAGCGGATTGCCA	300
Qy	346	ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTTCGGGCTGGAG	405
Db	301	ACCATGGAGGTCCGTATCAACGTATCGAGGCAGCAGGTAGAGAAAGTGTTTGGGCTGGAG	360
Qy	406	GAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC	465
Db	361	GAATACTGGTGCCAGTGCTGTGGCATGGAGCTCCTCGGGTACCACCAAAAGTCAGAAGGCC	420
Qy	466	TACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG	525
Db	421	TACATCCGGATTGCCTATTTGCGCAAGAACTTTGAGCAGGAGCCACTGGCCAAGGAAGTG	480
Qy	526	TCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGAGGGCATCCCTCCAGCCGAG	585
Db	481	TCACTGGAGCAAGGCATTGTACTACCTTGTCGCCCCCAGAAGGAATCCCCCAGCTGAG	540
Qy	586	GTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATC	645
Db	541	GTGGAGTGGCTTCGAAATGAGGACCTCGTGGACCCCTCCCTCGATCCCAATGTGTACATC	600
Qy	646	ACGCGGGAGCACAGCCTGGTGGTGCACAGGCCCGCCTTGCTGACACGGCCAACTACACC	705
Db	601	ACGCGGGAGCACAGCCTAGTCGTGCGTCAGGCCCGCCTGGCCGACACGGCCAACTACACC	660
Qy	706	TGCGTGGCCAAGAACATCGTGGCACGTGCGCCGACGCGCTCCGCTGCTGTATCGTCTAC	765

Db 661 TGTGTGGCCAAGAACATCGTAGCCCGTCGCCGAAGCACCTCTGCAGCGGTCATTGTTTAT 720  
 Qy 766 GTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGC 825  
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 Db 721 GTGAACGGTGGGTGGTTCGACGTGGACTGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGT 780  
 Qy 826 GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTC 885  
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 Db 841 TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACTCTGTGCCCAGTGGATGGGAGC 900  
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 Qy 1246 ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCAGCAAAGCAGACAACCCCCATCTGCTC 1305  
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 Db 1201 ACCTCGGGCTTCCAGCCTGTGAGCATCAAGCCAGCAAAGCAGACAACCCCCACCTGCTC 1260  
 Qy 1306 ACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG 1365  
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 Qy 1366 CAGGATGGGCCCAGCCCCAAGTTCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGT 1425  
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Qy	1606	ATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG	1665
Db	1561	ATACCCCGGATGCCATCCCGAGGAAAGATCTACGAGATCTACCTCACACTGCACAAG	1620
Qy	1666	CCGGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGC	1725
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Qy	1726	TGTGGACCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGG	1785
Db	1681	TGTGGGCCCCCAGGAGTCCTGCTCACCCGGCCAGTCATCCTTGCAATGGACCACTGTGGA	1740
Qy	1786	GAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG	1845
Db	1741	GAGCCCAGCCCTGACAGCTGGAGTCTGCGCCTCAAAAAGCAGTCCTGCGAGGGCAGTTGG	1800
Qy	1846	GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAG	1905
Db	1801	GAGGATGTGCTGCACCTTGGTGAGGAGTCACCTTCCCACCTCTACTACTGCCAGCTGGAG	1860
Qy	1906	GCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCC	1965
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Qy	1966	CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC	2025
Db	1921	CTCAGCGTGGCTGCCACCAAGCGCCTCAGGCTCCTTCTGTTTGCTCCCGTGGCCTGTACG	1980
Qy	2026	TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG	2085
Db	1981	TCCCTTGAGTACAACATCCGAGTGTAAGTGCCTACACGACACCCACGACGCTCTCAAGGAG	2040
Qy	2086	GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCAC	2145
Db	2041	GTGGTGCAGCTGGAGAAGCAGCTAGGTGGACAGCTGATCCAGGAGCCTCGCGTCCTGCAC	2100
Qy	2146	TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGG	2205
Db	2101	TTCAAAGACAGTTACCACAACCTACGTCTCTCCATCCACGACGTGCCAGCTCCCTGTGG	2160
Qy	2206	AAGAGTAAGCTCCTTGTGAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCAG	2265
Db	2161	AAGAGCAAGCTACTTGTGAGCTACCAGGAGATCCCTTTTACCACATCTGGAACGGCACC	2220
Qy	2266	CAGCGGTACTTGCACTGCACCTTACCCTGGAGCGTGTCAGCCCCAGCACTAGTGACCTG	2325
Db	2221	CAGCAGTATCTGCACTGCACCTTACCCTGGAGCGCATCAACGCCAGCACCAGCGACCTG	2280
Qy	2326	GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTC	2385
Db	2281	GCCTGCAAGGTGTGGGTGTGGCAGGTGGAGGGAGATGGGCAGAGCTTCAACATCAACTTC	2340
Qy	2386	AACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTC	2445
Db	2341	AACATCACTAAGGACACAAGGTTTGCTGAATTGTTGGCTCTGGAGAGTGAAGGGGGGGTC	2400

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RESULT 8

US-09-933-261-2

; Sequence 2, Application US/09933261

; Publication No. US20030040046A1

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; Leonardo, E. David

; Hink, Lindsay

; Masu, Masayuki

; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/933,261

; FILING DATE: 20-Aug-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/808,982

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: OSMAN, RICHARD A

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: UC96-217

; TELECOMMUNICATION INFORMATION:

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;          TELEPHONE: (415) 343-4341
;          TELEFAX: (415) 343-4342
;  INFORMATION FOR SEQ ID NO: 2:
;      SEQUENCE CHARACTERISTICS:
;          LENGTH: 1787 base pairs
;          TYPE: nucleic acid
;          STRANDEDNESS: double
;          TOPOLOGY: linear
;      MOLECULE TYPE: cDNA
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US-09-933-261-2

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Query Match          56.8%;  Score 1562.4;  DB 10;  Length 1787;
Best Local Similarity 98.5%;  Pred. No. 0;
Matches 1661;  Conservative 0;  Mismatches 16;  Indels 9;  Gaps 8;

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Qy	1789	CCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAG	1848
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Qy	1849	GATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCC	1908
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Qy	1909	AGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTC	1968
Db	838	 AGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTC	897
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Qy	2029	CTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTG	2088
Db	958	 CTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTG	1017
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Qy	2389	ATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCA	2448
Db	1315	 ATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCA	1374
Qy	2449	GCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTC	2508
Db	1375	 GCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTC	1434
Qy	2509	AGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCAGAACTCCAC	2568

Db 1435 AGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAACTCCAC 1494  
 Qy 2569 CTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAAC 2628  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1495 CTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAAC 1554  
 Qy 2629 CTGTGGGAGGCGCGGCACCTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCT 2688  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1555 CTGTGGGAGGCGCGGCACCTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCT 1614  
 Qy 2689 GGACTGGGCCAGCCAGACGCTGGCCTC-TTCACAGTG-TCGGAGGCTGAGTGCTGAGGCC 2746  
 || ||||| |||| ||| || ||||| ||||||||||||||||||||  
 Db 1615 GGGACTGGCCAGCAGGACGGTGGCTTCTTTTCACAGTGTCGGAGGCTGAGTGCTGAGGCC 1674  
 Qy 2747 GGCCAG 2752  
 |||||  
 Db 1675 GGCCAG 1680

RESULT 9

US-10-256-702-2

; Sequence 2, Application US/10256702

; Publication No. US20030059859A1

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; Leonardo, E. David

; Hink, Lindsay

; Masu, Masayuki

; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/256,702

; FILING DATE: 27-Sep-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/933,261

; FILING DATE: 20-Aug-2001

; APPLICATION NUMBER: 08/808,982

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: OSMAN, RICHARD A

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: UC96-217

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 343-4341  
; TELEFAX: (415) 343-4342  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1787 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-256-702-2

Query Match 56.8%; Score 1562.4; DB 15; Length 1787;  
Best Local Similarity 98.5%; Pred. No. 0;  
Matches 1661; Conservative 0; Mismatches 16; Indels 9; Gaps 8;

Qy	1070	GCAACTGTACCACTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCT	1129
Db	1	GCAACTGTACCACTGACCTCTG-GTACACACTGCTTCTGGCCCTGAGGACGTGGCCCTCT	59
Qy	1130	ATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCTGCTGCTTGTCTCATCCTCG	1189
Db	60	ATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCTGCTGCTTGTCTCATCCTCG	119
Qy	1190	TTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCT	1249
Db	120	TTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCT	179
Qy	1250	CAGGCTTCCAGCCCGTCAGCATC-AAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACC	1308
Db	180	CAGGCTTCCAGCCCGTCAGCATCTAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACC	239
Qy	1309	ATCCAGCCGGACCTCAGCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAG	1368
Db	240	ATCCAGCCGGACCTCAGCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAG	299
Qy	1369	GATGGGCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGC	1428
Db	300	GATGGGCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGC	359
Qy	1429	GGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGC	1488
Db	360	GGCCGCCACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGC	419
Qy	1489	CTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGG	1548
Db	420	CTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGG	479
Qy	1549	ACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATC	1608
Db	480	ACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGAATCAGCCTCCTCATC	539
Qy	1609	CCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCG	1668
Db	540	CCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCG	599
Qy	1669	GAAGACGTGAGGTTGCCCTAGCTGGCTGTGACACCCTGCTGAGTCCCATCGTTAGCTGT	1728

Db	600	 GAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGT	659
Qy	1729	GGACCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAG	1788
Db	660	 GGACCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAG	719
Qy	1789	CCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAG	1848
Db	720	 CCCAGCCCTGACAGCTGGAGCCTGGCCCTCAAAAAGCAGTCGTGCGAGGG-AGCTGGGAG	778
Qy	1849	GATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCC	1908
Db	779	 GATGT-CTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCC	837
Qy	1909	AGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTC	1968
Db	838	 AGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTC	897
Qy	1969	AGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCC	2028
Db	898	 AGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCC	957
Qy	2029	CTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTG	2088
Db	958	 CTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTG	1017
Qy	2089	GTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTC	2148
Db	1018	 GTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTT-	1076
Qy	2149	AAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAG	2208
Db	1077	 AAGGACAGTTACCACAACCT--GCCCTATCATCCACGATGTGCCCAGCTCCCTGTGGAAG	1134
Qy	2209	AGTAAGCTCCTTGTGCTAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAG	2268
Db	1135	 AGTAAGCTCCTTGTGCTAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAG	1194
Qy	2269	CGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCC	2328
Db	1195	 CGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCC	1254
Qy	2329	TGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAAC	2388
Db	1255	 TGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAAC	1314
Qy	2389	ATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCA	2448
Db	1315	 ATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCA	1374
Qy	2449	GCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCC	2508
Db	1375	 GCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCC	1434
Qy	2509	AGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCAC	2568

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Db      1435 AGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCAC 1494
Qy      2569 CTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAAC 2628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1495 CTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAAC 1554
Qy      2629 CTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCT 2688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1555 CTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCT 1614
Qy      2689 GGACTGGGCCAGCCAGACGCTGGCCTC-TTCACAGTG-TCGGAGGCTGAGTGCTGAGGCC 2746
          || ||||| ||| ||| || ||||||| ||||||||||||||||||||
Db      1615 GGGACTGGCCAGCAGGACGGTGGCTTCTTTACAGTGTTTCGGAGGCTGAGTGCTGAGGCC 1674
Qy      2747 GGCCAG 2752
          |||||
Db      1675 GGCCAG 1680

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RESULT 10

US-10-296-115-365

; Sequence 365, Application US/10296115

; Publication No. US20040053248A1

; GENERAL INFORMATION:

; APPLICANT: Hyseq Inc

; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides

; FILE REFERENCE: 784PCT

; CURRENT APPLICATION NUMBER: US/10/296,115

; CURRENT FILING DATE: 2002-11-18

; PRIOR APPLICATION NUMBER: US09/488,725

; PRIOR FILING DATE: 2000-01-21

; PRIOR APPLICATION NUMBER: US09/552,317

; PRIOR FILING DATE: 2000-04-25

; NUMBER OF SEQ ID NOS: 1478

; SEQ ID NO 365

; LENGTH: 1321

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-296-115-365

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Query Match          43.8%; Score 1206.6; DB 13; Length 1321;
Best Local Similarity 98.0%; Pred. No. 1.6e-296;
Matches 1295; Conservative 0; Mismatches 19; Indels 7; Gaps 7;

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Qy      1435 CACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCC 1494
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1   CACACACTGCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCC 60
Qy      1495 ACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTC 1554
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61  ACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTC 120
Qy      1555 AACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCA 1614
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 AACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGAATCAGCCTCCTCATCCCCCA 180
Qy      1615 GATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGAC 1674

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Db	181	 GATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGAC	240
Qy	1675	GTGAGGTTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCC	1734
Db	241	 GTGAGGTTGCCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCC	300
Qy	1735	CCT-GGCGTCCTGCTCACCCGGCCAGTCATCCT-GGCTATGGACCACTGT-GGGGAGCCC	1791
Db	301	 CCTGGGCGTCCTGCTTACCCGGCCAGTCATCCTGGGGTATGGACCACTGTGGGGGAGCCC	360
Qy	1792	AGCCCTGACAGCT-GGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGA	1850
Db	361	 AGCCCTGACAGCTGGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGA	420
Qy	1851	TGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAG	1910
Db	421	 TGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAG	480
Qy	1911	TGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAG	1970
Db	481	 TGCCTGCTACGTCTTCACCGAGCAGCTGAGCCGCTATGCCCTGGTGGGAGAGGCCCTCAG	540
Qy	1971	CGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCT	2030
Db	541	 CGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCT	600
Qy	2031	CGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGT	2090
Db	601	 CGAGTACAACATACTGGTCTACTGCCTGCATGACACTCACGATGCACTCAACGTAGTGGT	660
Qy	2091	GCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTCAA	2150
Db	661	 GCAGCTGGAGAAGCAGCTGCAGGGACAGCTGATCCAGGAGCCACTGGTACTGCACTTCAA	720
Qy	2151	GGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAG	2210
Db	721	 GGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAG	780
Qy	2211	TAAGCTCCTTGTGCTAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCG	2270
Db	781	 TAAGCTCCTTGTGCTAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCG	840
Qy	2271	GTA CTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTG	2330
Db	841	 GTA CTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTG	900
Qy	2331	CAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACAT	2390
Db	901	 CAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACAT	960
Qy	2391	CACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGC	2450
Db	961	 CACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGC	1020
Qy	2451	CCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAG	2510

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Db      1021 CCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCTCATTCGGCAGAAGATAATTTCCAG 1080
Qy      2511 CCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCT 2570
          |||
Db      1081 CCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCT 1140
Qy      2571 GGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCT 2630
          |||
Db      1141 GGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCT 1200
Qy      2631 GTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCT-G 2689
          |||
Db      1201 GTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGG 1260
Qy      2690 GACTGGGCCAGCCAGACGCTGGCCTC-TTCACAGTG-TCGGAGGCTGAGTGCTGAGGCCG 2747
          |||
Db      1261 GACTGGGCCAGCAGGACGGTGGCTTCTTTCACAGTGTTTCGGAGGCTGAGTGCTGAGGCCG 1320
Qy      2748 G 2748
          |
Db      1321 G 1321

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RESULT 11

US-09-833-381-1806

; Sequence 1806, Application US/09833381

; Patent No. US20020132090A1

; GENERAL INFORMATION:

; APPLICANT: Robison, Keith E.

; TITLE OF INVENTION: No. US20020132090A1e1 Nucleic Acid and Protein Homologs

; FILE REFERENCE: 5800-119

; CURRENT APPLICATION NUMBER: US/09/833,381

; CURRENT FILING DATE: 2001-04-11

; PRIOR APPLICATION NUMBER: 09/516,448

; PRIOR FILING DATE: 2000-02-29

; NUMBER OF SEQ ID NOS: 2050

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 1806

; LENGTH: 1282

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (1)...(1282)

; OTHER INFORMATION: n = A,T,C or G

US-09-833-381-1806

Query Match 42.0%; Score 1155.8; DB 9; Length 1282;

Best Local Similarity 98.2%; Pred. No. 1.3e-283;

Matches 1263; Conservative 0; Mismatches 13; Indels 10; Gaps 9;

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Qy      1469 CCGAGGAGTTCGTCTCCCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCA 1528
          |||
Db      1    CCGAGGAGTTCGTCTCCCGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCA 60
Qy      1529 CCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATA 1588
          |||

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Db	61	CCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATA	120
Qy	1589	CAGGTATCAGCCTCCTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCT	1648
Db	121	CAGGAATCAGCCTCCTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCT	180
Qy	1649	ACCTCACGCTGCACAAGCCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGC	1708
Db	181	ACCTCACGCTGCACAAGCCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGC	240
Qy	1709	TGAGTCCCATCGTTAGCTGTGGACCCCCT-GGCGTCCTGCTCACCCGGCCAGTCATCCT-	1766
Db	241	TGAGTCCCATCGTTAGCTGTGGACCCCCTGGGCGTCCTGCTCACCCGGCCAGTCATCCTG	300
Qy	1767	GGCTATGGACCACTGTGGGGAGCCCAGCCCTGACAGCT-GGAGCCTGCGCCTCAAAAAGC	1825
Db	301	GGGTATGGACCACTGTGGGGAGCCCAGCCCTGACAGCTGGGAGCCTGCGCCTCAAAAAGC	360
Qy	1826	AGTCGTGCGAGGGCAGCTGGGAGGATGTGC-TGCACCTGGGCGAGGAGGCGCCCTCCCAC	1884
Db	361	AGTCGTGCGAGGGCAGCTGGGAGGATGTGCTTGCACCTGGGCGAGGAGGCGCCCTCCCAC	420
Qy	1885	CTCTACTACTGCCAGCTGGAGGCCAGTGCCCTGCTACGTCTTCACCGAGCAGCTGGGCCGC	1944
Db	421	CTCTACTACTGCCAGCTGGAGGCCAGTGCCCTGCTACGTCTTCACCGAGCAGCTGAGCCGC	480
Qy	1945	TTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTG	2004
Db	481	TATGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTG	540
Qy	2005	TTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGAC	2064
Db	541	TTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACATACTGGTCTACTGCCTGCATGAC	600
Qy	2065	ACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATC	2124
Db	601	ACTCACGATGCACTCAACGTAGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATC	660
Qy	2125	CAGGAGCCACGGGTCTCTGCACTTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCAC	2184
Db	661	CAGGAGCCACGGGTCTCTGCACTTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCAC	720
Qy	2185	GATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTT	2244
Db	721	GATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTT	780
Qy	2245	TATCACATCTGGAATGGCACGCAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTC	2304
Db	781	TATCACATCTGGAATGGCACGCAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTC	840
Qy	2305	AGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGG	2364
Db	841	AGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGG	900
Qy	2365	CAGAGCTTCAGCATCAACTTCAACATCACCAGGACACAAGGTTTGCTGAGCTGCTGGCT	2424
Db	901	CAGAGCTTCAGCATCAACTTCAACATCACCAGGACACAAGGTTTGCTGAGCTGCTGGCT	960

Qy 2425 CTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTC 2484  
 |||  
 Db 961 CTGGAGAGTGAAGCGNGGGTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTC 1020  
 Qy 2485 CTCATTGCGCAGAAGATAA-TTTCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTG 2543  
 |||  
 Db 1021 CTCATTGCGCAGAAGATAATTTTCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTG 1080  
 Qy 2544 GCGG-ACTCTGGCCCAGAACTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGC 2602  
 |||  
 Db 1081 GCGGAACCTCTGGCCCAGAACTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGC 1140  
 Qy 2603 CCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACC 2662  
 |||  
 Db 1141 CCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACC 1200  
 Qy 2663 TCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAG 2722  
 |||  
 Db 1201 TCAGCCAGCTGG-TGCAGCAGTGGCTGGACTGGGC--AGCAGACGCTGG-CTCTTCACAG 1256  
 Qy 2723 TGTCGGAGGCTGAGTGCTGAGGCCGG 2748  
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 Db 1257 TGTCGGAGGCTGAGTGCTGAGGCCGG 1282

RESULT 12

US-10-087-684-1

; Sequence 1, Application US/10087684

; Publication No. US20040029116A1

; GENERAL INFORMATION:

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: MacDougall, John R.

; APPLICANT: Millet, Isabelle

; APPLICANT: Ellerman, Karen

; APPLICANT: Stone, David J.

; APPLICANT: Grosse, William M.

; APPLICANT: Lepley, Denise M.

; APPLICANT: Rieger, Daniel K.

; APPLICANT: Burgess, Cathereine E.

; APPLICANT: Casman, Stacie, J.

; APPLICANT: Spytek, Kimberly A.

; APPLICANT: Boldog, Ferenc L.

; APPLICANT: Li, Li

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Mishra, Vishnu

; APPLICANT: Shenoy, Suresh G.

; APPLICANT: Rastelli, Luca

; APPLICANT: Tchernev, Velizar T.

; APPLICANT: Vernet, Corine A.M.

; APPLICANT: Zerhusen, Bryan D.

; APPLICANT: Malyankar, Uriel M.

; APPLICANT: Guo, Xiaojia

; APPLICANT: Miller, Charles E.

; APPLICANT: Gangolli, Esha A.

; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: 21402-214 CIP

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; CURRENT APPLICATION NUMBER: US/10/087,684
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 1
; LENGTH: 2860
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (59)..(2857)
US-10-087-684-1

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Query Match          34.0%; Score 936.2; DB 13; Length 2860;
Best Local Similarity 61.7%; Pred. No. 9e-228;
Matches 1662; Conservative 0; Mismatches 938; Indels 93; Gaps 7;

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Qy      143 ACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATG 202
        || | | || | | | | | | | | | | | | | | | | | | |
Db      168 ACTCCTTCCCGTCAGCGCCAGCAGAGCCGCTGCCCTACTTCCTGCAGGAGCCACAGGACG 227

Qy      203 TGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGA 262
        || || | | | | | | | | | | | | | | | | | | | |
Db      228 CCTACATTGTGAAGAACAAGCCTGTGGAGCTCCGCTGCCGCGCCTTCCCGCCACACAGA 287

Qy      263 TCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCA 322
        || | | | | | | | | | | | | | | | | | | | | | |
Db      288 TCTACTTCAAGTGCAACGGCGAGTGGGTGAGCCAGAACGACCACGTACACAGGAAGGCC 347

Qy      323 CAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGG 382
        || | | | | | | | | | | | | | | | | | | | | | |
Db      348 TGGATGAGGCCACCGGTCTGCGGGTGCGCGAGGTGCAGATCGAGGTGTCGCGGCAGCAGG 407

Qy      383 TCGAGAAGGTGTTTCGGGCTGGAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGG 442
        | | | | | | | | | | | | | | | | | | | | | | | |
Db      408 TGGAGGAGCTCTTTGGGCTGGAGGATTACTGGTGCCAGTGCGTGGCCTGGAGCTCCGCGG 467

Qy      443 GCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGC 502
        || || | | | | | | | | | | | | | | | | | | | |
Db      468 GCACCACCAAGAGTCGCGGAGCCTACGTCCGCATCGCCTACCTGCGCAAGAACTTCGATC 527

Qy      503 AGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCAC 562
        || || | | | | | | | | | | | | | | | | | | | |
Db      528 AGGAGCCTCTGGGCAAGGAGGTGCCCTGGACCATGAGGTTCTCCTGCAGTGCCGCCCCGC 587

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Qy	563	CGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGT	622
Db	588	CGGAGGGGGTGCCTGTGGCCGAGGTGGAATGGCTCAAGAATGAGGATGTCATCGACCCCA	647
Qy	623	CCCTGGACCCCAATGTATACATCACGCGGGAGCACAGCCTGGTGGTGGCAGGCCCCGCC	682
Db	648	CCCAGGACACCAACTTCCTGCTCACCATCGACCACAACCTCATCATCCGCCAGGCCCCGCC	707
Qy	683	TTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAATCGTGGCAGCTCGCCGAGCG	742
Db	708	TGTCGGACACTGCCAACTATACCTGCGTGGCCAAGAATCGTGGCCAAACGCCGGAGCA	767
Qy	743	CCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGGTGCAGCTGGACCGAGTGGTCCG	802
Db	768	CCACTGCCACCGTATCGTCTACGTGAATGGCGGCTGGTCCAGCTGGGCAGAGTGGTCAC	827
Qy	803	TCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGG	862
Db	828	CCTGCTCCAACCGCTGTGGCCGAGGCTGGCAGAAGCGCACCCGGACCTGCACCAACCCCG	887
Qy	863	CGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCA	922
Db	888	CTCCACTCAACGGAGGGGCGCTTCTGCGAGGGCCAGGCATTCAGAAGACCGCCTGCACCA	947
Qy	923	CCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTTCGGCCTGTGGGCTGG	982
Db	948	CCATCTGCCCAGTCGATGGGGCGTGGACGGAGTGGAGCAAGTGGTTCAGCCTGCAGCACTG	1007
Qy	983	ACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCAGCACCCCCGAACGGAGGGGAGG	1042
Db	1008	AGTGTGCCCACTGGCGTAGCCGCGAGTGCATGGCGCCCCCAGGAGGAGGAGGAGG	1067
Qy	1043	AGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTG	1102
Db	1068	ACTGCAGCGGGACGCTGCTCGACTCTAAGAACTGCACAGATGGGCTGTGCATGCAACTGG	1127
Qy	1103	CTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGG	1162
Db	1128	AGGCCTCAGGGGATGCGGCGCTGTATGCGGGGCTCGTGGTGGCCATCTTCGTGGTCTGG	1187
Qy	1163	TCCTGCTGCTGCTTGTCTCATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAG	1222
Db	1188	CAATCCTCATGGCGGTGGGGGTGGTGGTGTACCGCCGCAACTGCCGTGACTTCGACACAG	1247
Qy	1223	ATGTGGCTGACTCGTCCATT---CTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCA	1279
Db	1248	ACATCACTGACTCATCTGCTGCCCTGACTGGTGGTTTCCACCCCGTCAACTTTAAGACGG	1307
Qy	1280	GCAAAGCAGACAACCCCATCTGCT-----CACCATCCAGCCGGACCTCAGCACCACCA	1333
Db	1308	CAAGGCCAGTAACCCGAGCTCCTACACCCCTCTGTGCCTCCTGACCTGACAGCCAGCG	1367
Qy	1334	CCACCACCTACCAGGGCAGTCTCTGT'CCCCGGCAGGA-----	1370
Db	1368	CCGGCATCTACCGCGGACCCGTGTATGCCCTGCAGGACTCCACCGACAAAATCCCCATGA	1427
Qy	1371	-----TGGGCCCAGCCCCAAGTTCCAGCTCACCA-----	1399

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Db      1428 CCAACTCTCCTCTGCTGGACCCCTTACCCAGCCTTAAGGTCAAGGTCTACAGCTCCAGCA 1487

Qy      1400 --ATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACAC-----ACTGCACC 1447
          | ||| | | ||| || | | ||| | | | | | |
Db      1488 CCACGGGCTCTGGGCCAGGCCTGGCAGATGGGGCTGACCTGCTGGGGGTCTTGCCGCCTG 1547

Qy      1448 ACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAGAATACT 1507
          || | ||| | | ||| || | ||| | | | | | |
Db      1548 GCACATACCCTAGCGATTTGCCCCGGGACACCCACTTCCTGCACCTGCGCAGCGCCAGCC 1607

Qy      1508 TCCGCTC-----CCTGCCCGGAGGCACCAGCAACATGACCTATGGGACCT 1552
          || | || | ||||| ||| | | | | | | || |||
Db      1608 TCGGTTCCCAGCAGCTCTTGGGCCTGCCCGGAGACCCAGGGAGCAGCGTCAGCGGCACCT 1667

Qy      1553 TCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCC 1612
          | || ||| || || |||| | |||| | |||| | || | |||
Db      1668 TTGGCTGCCTGGGTGGGAGGCTCAGCATCCCCGGCACAGGGGTGAGTTGCTGGTGCCCA 1727

Qy      1613 CAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAG 1672
          | |||| | ||| || ||| ||| |||| | || | |||| | |||
Db      1728 ATGGAGCCATTCCCCAGGGCAAGTTCTACGAGATGTATCTACTCATCAACAAGGCAGAAA 1787

Qy      1673 ACGTGAGGTTGCCCTAGCTGGCTGTGACACCCTGCTGAGTCCCATCGTTAGCTGTGGAC 1732
          | || || || || |||| | |||| ||| || | |||||
Db      1788 GTACCCTGCCGCTTTCAGAAGGGACCCAGACAGTATTGAGCCCCCTCGGTGACCTGTGGAC 1847

Qy      1733 CCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCA 1792
          || | || ||||| || || ||||| | || ||||| || ||
Db      1848 CCACAGGCCTCCTGCTGTGCGCCCCGTGATCCTCACCATGCCCCACTGTGCCGAAGTCA 1907

Qy      1793 GCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATG 1852
          | | |||| | | | |||| | || | | |||| | |||||
Db      1908 GTGCCCCGTGACTGGATCTTTCAGCTCAAGACCCAGGCCACCAGGGCCACTGGGAGGAGG 1967

Qy      1853 TGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTG 1912
          || || |||| | |||| | | | | ||||| ||||| |||| |
Db      1968 TGGTGACCCTGGATGAGGAGACCCTGAACACACCCTGCTACTGCCAGCTGGAGCCCAGGG 2027

Qy      1913 CCTGCTACGTCTTCACCGAGCAGCTGGGCGCCTTTGCCCTGGTGGGAGAGGCCCTCAGCG 1972
          |||| || || | || ||||| || | | || |||| |
Db      2028 CCTGTCACATCCTGCTGGACCAGCTGGGCACCTACGTGTTACGGGCGAGTCCTATTCCC 2087

Qy      1973 TGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCG 2032
          | || | |||| | || |||| | || || | | |||||
Db      2088 GCTCAGCAGTCAAGCGGCTCCAGCTGGCCGTCTTCGCCCCCGCCCTCTGCACCTCCCTGG 2147

Qy      2033 AGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGC 2092
          ||||| | ||||| ||||| || |||| | | |||| | |||
Db      2148 AGTACAGCCTCCGGGTCTACTGCCTGGAGGACACGCCTGTAGCACTGAAGGAGGTGCTGG 2207

Qy      2093 AGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGG 2152
          ||||| | |||| ||| | || | ||||| || |||||
Db      2208 AGCTGGAGCGGACTCTGGGCGGATACTTGGTGGAGGAGCCGAAACCGCTAATGTTCAAGG 2267

Qy      2153 ACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGGAAGAGTA 2212
          ||||| ||||| ||||| || || || | ||| ||| ||| |||

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Db 2268 ACAGTTACCACAACCTGCGCCTCTCCCTCCATGACCTCCCCCATGCCCATTGGAGGAGCA 2327  
 Qy 2213 AGCTCCTTGTCTAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGT 2272  
 |||| || || || ||||| ||||| ||||| ||||| ||||| |||||  
 Db 2328 AGCTGCTGGCCAAATACCAGGAGATCCCCTTCTATCACATTTGGAGTGGCAGCCAGAAGG 2387  
 Qy 2273 ACTTGCACTGCACCTTCACCCCTGGAGCGTGTCTAGCCCCAGCACTAGTGACCTGGCCTGCA 2332  
 | | ||||| ||||| ||||| | |||| | | | |||||  
 Db 2388 CCCTCCACTGCACTTTACCCCTGGAGAGGCACAGCTTGGCCTCCACAGAGCTCACCTGCA 2447  
 Qy 2333 AGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCA 2392  
 || | || |||| |||| |||| || || || |||| |||| | | || ||  
 Db 2448 AGATCTGCGTGCGGCAAGTGAAGGGGAGGGCCAGATATTCCAGCTGCATACCACTCTGG 2507  
 Qy 2393 CCAAG---GACACAAGGTTTGTCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAG 2449  
 | || | | | || || | || || |||||  
 Db 2508 CAGAGACACCTGCTGGCTCCCTGGACACTCTCTGCTCTGCCCCCTGGCAGCACTGTACCA 2567  
 Qy 2450 CCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCA 2509  
 ||| | |||| || ||||| ||||| | |||| ||||| ||||| |||||  
 Db 2568 CCCAGCTGGGACCTTATGCCTTCAAGATCCCCTGTCCATCCGCCAGAAGATATGCAACA 2627  
 Qy 2510 GCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACC 2569  
 |||| || | |||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 2628 GCCTAGATGCCCCCAACTCACGGGGCAATGACTGGCGGATGTTAGCACAGAAGCTCTCTA 2687  
 Qy 2570 TGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACC 2629  
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 Db 2688 TGGACCGGTACCTGAATTACTTTGCCACCAAAGCGAGCCCCACGGGTGTGATCCTGGACC 2747  
 Qy 2630 TGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTG 2689  
 | |||| || | || | | || || ||||| | |||| || |||||  
 Db 2748 TCTGGGAAGCTCTGCAGCAGGACGATGGGGACCTCAACAGCCTGGCGAGTGCCTTGGAGG 2807  
 Qy 2690 GACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCTGGAGGCTGAGTGTCTGA 2742  
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 Db 2808 AGATGGGCAAGAGTGAGATGCTGGTGGCTGTGGCCACCGACGGGGACTGCTGA 2860

RESULT 13

US-10-087-684-3

; Sequence 3, Application US/10087684

; Publication No. US20040029116A1

; GENERAL INFORMATION:

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: MacDougall, John R.

; APPLICANT: Millet, Isabelle

; APPLICANT: Ellerman, Karen

; APPLICANT: Stone, David J.

; APPLICANT: Grosse, William M.

; APPLICANT: Lepley, Denise M.

; APPLICANT: Rieger, Daniel K.

; APPLICANT: Burgess, Cathereine E.

; APPLICANT: Casman, Stacie, J.

; APPLICANT: Spytek, Kimberly A.

; APPLICANT: Boldog, Ferenc L.

; APPLICANT: Li, Li



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; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles E.
; APPLICANT: Gangolli, Esha A.
; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-214 CIP
; CURRENT APPLICATION NUMBER: US/10/087,684
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 3
; LENGTH: 2860
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (59)..(2857)
US-10-087-684-3

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Query Match          34.0%; Score 936.2; DB 13; Length 2860;
Best Local Similarity 61.7%; Pred. No. 9e-228;
Matches 1662; Conservative 0; Mismatches 938; Indels 93; Gaps 7;

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Qy      143 ACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATG 202
          || | | || | | | | | | | | | | | | | | | | | | | | | |
Db      168 ACTCCTTCCCGTCAGCGCCAGCAGAGCCGCTGCCCTACTTCCTGCAGGAGCCACAGGACG 227

Qy      203 TGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGA 262
          || || | | | | | | | | | | | | | | | | | | | | | | |
Db      228 CCTACATTGTGAAGAACAAGCCTGTGGAGCTTCGCTGCCGCGCCTTCCCCGCCACACAGA 287

Qy      263 TCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCA 322
          || | | | | | | | | | | | | | | | | | | | | | | | |
Db      288 TCTACTTCAAGTGCAACGGCGAGTGGGTGAGCCAGAACGACCACGTACACAGGAAGGCC 347

Qy      323 CAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGG 382
          || | | | | | | | | | | | | | | | | | | | | | | |
Db      348 TGGATGAGGCCACCGCCTGCGGGTGCGCGAGGTGCAGATCGAGGTGTCGCGGCAGCAGG 407

```

Qy 383 TCGAGAAGGTGTTTCGGGCTGGAGGAATACTGGTGCCAGTGCCTGGCATGGAGCTCCTCGG 442  
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 Db 408 TGGAGGAGCTCTTTGGGCTGGAGGATTACTGGTGCCAGTGCCTGGCCTGGAGCTCCGCAG 467  
 Qy 443 GCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGC 502  
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 Db 468 GCACCACCAAGAGTCGCCGAGCCTACGTCCGCATCGCCTACCTGCGCAAGAACTTCGATC 527  
 Qy 503 AGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCAC 562  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 528 AGGAGCCTCTGGGCAAGGAGGTGCCCTGGACCATGAGGTTCTCCTGCAGTGCCGCCCGC 587  
 Qy 563 CGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGT 622  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 588 CGGAGGGGTGCCTGTGGCCGAGGTGGAATGGCTCAAGAATGAGGATGTCATCGACCCCA 647  
 Qy 623 CCCTGGACCCCAATGTATACATCACGCGGGAGCACAGCCTGGTGGTGCACAGGCCCGCC 682  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 648 CCCAGGACACCAACTTCCTGCTCACCATCGACCACAACCTCATCATCGCCAGGCCCGCC 707  
 Qy 683 TTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAACATCGTGGCACGTCGCCGCAGCG 742  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 708 TGTCGGACACTGCCAACTATACCTGCGTGGCCAAGAACATCGTGGCCAAACGCCGGAGCA 767  
 Qy 743 CCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCG 802  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 768 CCACTGCCACCGTCATCGTCTACGTGAATGGCGGCTGGTCCAGCTGGGCAGAGTGGTCAC 827  
 Qy 803 TCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGG 862  
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 Db 828 CCTGCTCCAACCGCTGTGGCCGAGGCTGGCAGAAGCGCACCCGGACCTGCACCAACCCCG 887  
 Qy 863 CGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCA 922  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 888 CTCCACTCAACGGAGGGGCTTCTGCGAGGGCCAGGCATTCCAGAAGACCGCTGCACCA 947  
 Qy 923 CCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTTCGGCCTGTGGGCTGG 982  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 948 CCATCTGCCCAGTCGATGGGGCGTGGACGGAGTGGAGCAAGTGGTCAGCCTGCAGCACTG 1007  
 Qy 983 ACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGG 1042  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1008 AGTGTGCCCACTGGCGTAGCCGCGAGTGCATGGCGCCCCACCCAGAACGGAGGCCGTG 1067  
 Qy 1043 AGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTG 1102  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1068 ACTGCAGCGGGACGCTGCTCGACTCTAAGAACTGCACAGATGGGCTGTGCATGCAACTGG 1127  
 Qy 1103 CTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGG 1162  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1128 AGGCCTCAGGGGATGCGGCGCTGTATGCGGGCTCGTGGTGGCCATCTTCGTGGTTCGTGG 1187  
 Qy 1163 TCCTGCTGCTGCTTGTCTCATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAG 1222  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 1188 CAATCCTCATGGCGGTGGGGGTGGTGGTGTACCGCCGCAACTGCCGTGACTTCGACACAG 1247

Qy	1223	ATGTGGCTGACTCGTCCATT---CTCACCTCAGGCTTCAGCCCGTCAGCATCAAGCCCCA	1279
Db	1248	ACATCACTGACTCATCTGCTGCCCTGACTGGTGGTTTCCACCCCGTCAACTTTAAGACGG	1307
Qy	1280	GCAAAGCAGACAACCCCCATCTGCT-----CACCATCCAGCCGGACCTCAGCACCACCA	1333
Db	1308	CAAGGCCCAGTAACCCGCAGCTCCTACACCCCTCTGTGCCTCCTGACCTGACAGCCAGCG	1367
Qy	1334	CCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGA-----	1370
Db	1368	CCGGCATCTACCGCGGACCCGTGTATGCCCTGCAGGACTCCACCGACAAAATCCCCATGA	1427
Qy	1371	-----TGGGCCAGCCCCAAGTTCAGCTCACCA-----	1399
Db	1428	CCA ACTCTCCTCTGCTGGACCCCTTACCCAGCCTTAAGGTCAAGGTCTACAGCTCCAGCA	1487
Qy	1400	--ATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACAC-----ACTGCACC	1447
Db	1488	CCACGGGCTCTGGGCCAGGCCTGGCAGATGGGGCTGACCTGCTGGGGGTCTTGCCGCCTG	1547
Qy	1448	ACAGCTCTCCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAGA ACTACT	1507
Db	1548	GCACATACCCTAGCGATTTGCCCCGGGACACCCACTTCCTGCACCTGCGCAGCGCCAGCC	1607
Qy	1508	TCCGCTC-----CCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCT	1552
Db	1608	TCGGTTC C CAGCAGCTCTTGGGCCCTGCCCCGAGACCCAGGGAGCAGCGTCAGCGGCACCT	1667
Qy	1553	TCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCC	1612
Db	1668	TTGGCTGCCTGGGTGGGAGGCTCAGCATCCCCGGGCACAGGGGTGAGCTTGCTGGTGCCCA	1727
Qy	1613	CAGATGCCATAACCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAG	1672
Db	1728	ATGGAGCCATTCCCCAGGGCAAGTTCTACGAGATGTATCTACTCATCAACAAGGCAGAAA	1787
Qy	1673	ACGTGAGGTTGCCCCTAGCTGGCTGTGACCCCTGCTGAGTCCCATCGTTAGCTGTGGAC	1732
Db	1788	GTACCCTGCCGCTTTCAGAAGGGACCCAGACAGTATTGAGCCCCTCGGTGACCTGTGGAC	1847
Qy	1733	CCCCTGGCGTCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCCA	1792
Db	1848	CCACAGGCCTCCTGCTGTGCCGCCCGTCATCCTCACCATGCCCCACTGTGCCGAAGTCA	1907
Qy	1793	GCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATG	1852
Db	1908	GTGCCCGTGACTGGATCTTTAGCTCAAGACCCAGGCCACCAGGGCCACTGGGAGGAGG	1967
Qy	1853	TGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTG	1912
Db	1968	TGGTGACCCTGGATGAGGAGACCCCTGAACACACCCTGCTACTGCCAGCTGGAGCCCAGGG	2027
Qy	1913	CCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCG	1972
Db	2028	CCTGTACATCCTGCTGGACCAGCTGGGCACCTACGTGTTACGGGCGAGTCTATTTCC	2087
Qy	1973	TGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTTGCGCCGGTGGCCTGCACCTCCCTCG	2032

Db	2088	GCTCAGCAGTCAAGCGGCTCCAGCTGGCCGCTCTCGCCCCGCCCTCTGCACCTCCCTGG	2147
Qy	2033	AGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGC	2092
Db	2148	AGTACAGCCTCCGGGTCTACTGCCTGGAGGACACGCCTGTAGCACTGAAGGAGGTGCTGG	2207
Qy	2093	AGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTCAAGG	2152
Db	2208	AGCTGGAGCGGACTCTGGGCGGATACTTGGTGGAGGAGCCGAAACCGCTAATGTTCAAGG	2267
Qy	2153	ACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTA	2212
Db	2268	ACAGTTACCACAACCTGCGCCTCTCCCTCCATGACCTCCCCCATGCCATTGGAGGAGCA	2327
Qy	2213	AGCTCCTTGTGCTAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCAGCGCGGT	2272
Db	2328	AGCTGCTGGCCAAATACCAGGAGATCCCCTTCTATCACATTTGGAGTGGCAGCCAGAAGG	2387
Qy	2273	ACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCA	2332
Db	2388	CCCTCCACTGCACCTTCACCCTGGAGAGGCACAGCTTGGCCTCCACAGAGCTCACCTGCA	2447
Qy	2333	AGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCA	2392
Db	2448	AGATCTGCGTGCGGCAAGTGAAGGGGAGGGCCAGATATTCCAGCTGCATACCACTCTGG	2507
Qy	2393	CCAAG---GACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGTCCCAG	2449
Db	2508	CAGAGACACCTGCTGGCTCCCTGGACACTCTCTGCTCTGCCCCTGGCAGCACTGTCACCA	2567
Qy	2450	CCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCTCATTTCGGCAGAAGATAATTTCCA	2509
Db	2568	CCAGCTGGGACCTTATGCCTTCAAGATCCCACTGTCCATCCGCCAGAAGATATGCAACA	2627
Qy	2510	GCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACC	2569
Db	2628	GCCTAGATGCCCCCAACTCACGGGGCAATGACTGGCGGATGTTAGCACAGAAGCTCTCTA	2687
Qy	2570	TGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACC	2629
Db	2688	TGGACCGGTACCTGAATTACTTTGCCACCAAAGCGAGCCCCACGGGTGTGATCCTGGACC	2747
Qy	2630	TGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTG	2689
Db	2748	TCTGGGAAGCTCTGCAGCAGGACGATGGGGACCTCAACAGCCTGGCGAGTGCCTTGGAGG	2807
Qy	2690	GACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTGCGAGGCTGAGTGTGA	2742
Db	2808	AGATGGGCAAGAGTGAGATGCTGGTGGCTGTGGCCACCGACGGGGACTGCTGA	2860

RESULT 14

US-10-218-779-1

; Sequence 1, Application US/10218779

; Publication No. US20040029222A1

; GENERAL INFORMATION:

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; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise
; APPLICANT: Rieger, Daniel
; APPLICANT: Burgess, Catherine
; APPLICANT: Casman, Stacie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Patturajan, Meera
; APPLICANT: Shenoy, Suresh
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Malyankar, Uriel
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles
; APPLICANT: Gangolli, Esha
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-214
; CURRENT APPLICATION NUMBER: US/10/218,779
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,-926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2860
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-218-779-1

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Query Match          34.0%; Score 936.2; DB 13; Length 2860;
Best Local Similarity 61.7%; Pred. No. 9e-228;
Matches 1662; Conservative 0; Mismatches 938; Indels 93; Gaps 7;

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Qy      143 ACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATG 202
          || | | ||      | | | | || | || | || | || | || | || | || |
Db      168 ACTCCTTCCCGTCAGCGCCAGCAGAGCCGCTGCCCTACTTCCTGCAGGAGCCACAGGACG 227

```

Qy 203 TGTACATCGTCAAGAACAAGCCAGTGTGCTTGTGTGCAAGGCCGTGCCCCGCCACGCAGA 262  
 ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 228 CCTACATTGTGAAGAACAAGCCTGTGGAGCTCCGCTGCCGCGCCTTCCCCGCCACACAGA 287

Qy 263 TCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCA 322  
 ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 288 TCTACTTCAAGTGCAACGGCGAGTGGGTGAGCCAGAACGACCACGTACACAGGAAGGCC 347

Qy 323 CAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGG 382  
 || | | || || ||||| ||||| | || | || || ||||| |||||  
 Db 348 TGGATGAGGCCACCGGTCTGCGGGTGCAGGAGGTGCAGATCGAGGTGTGCGGGCAGCAGG 407

Qy 383 TCGAGAAGGTGTTGCGGCTGGAGGAATACTGGTGCCAGTGCCTGGCATGGAGCTCCTCGG 442  
 | ||| || | || ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 408 TGGAGGAGCTCTTTGGGCTGGAGGATTACTGGTGCCAGTGCCTGGCCTGGAGCTCCGCGG 467

Qy 443 GCACCACCAAGAGTCAGAAGGCCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGC 502  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 468 GCACCACCAAGAGTCGCCGAGCCTACGTCCGCATCGCCTACCTGCGCAAGAACTTCGATC 527

Qy 503 AGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCAC 562  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 528 AGGAGCCTCTGGGCAAGGAGGTGCCCTGGACCATGAGGTTCTCCTGCAGTGCCGCCCGC 587

Qy 563 CGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGT 622  
 ||||| | ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 588 CGGAGGGGTGCCTGTGGCCGAGGTGGAATGGCTCAAGAATGAGGATGTCATCGACCCCA 647

Qy 623 CCCTGGACCCCAATGTATACATCACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCC 682  
 ||| |||| |||| | |||| || |||| |||| | | || ||||| |||||  
 Db 648 CCCAGGACACCAACTTCTGCTCACCATCGACCACAACCTCATCATCCGCCAGGCCCGCC 707

Qy 683 TTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAACATCGTGGCACGTGCGCCGAGCG 742  
 | | |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 708 TGTCGGACACTGCCAACTATACCTGCGTGGCCAAGAACATCGTGGCCAAGCGCCGAGCA 767

Qy 743 CCTCCGCTGCTGTCTACGTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCCG 802  
 || | || | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 768 CCACTGCCACCGTCATCGTCTACGTGAATGGCGGCTGGTCCAGCTGGGCAGAGTGGTCAC 827

Qy 803 TCTGCAGCGCCAGCTGTGGGCGCGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGG 862  
 |||| | | ||||| || ||||| ||||| || ||||| ||||| ||||| |||||  
 Db 828 CCTGCTCCAACCGCTGTGGCCGAGGCTGGCAGAAGCGCACCCGGACCTGCACCAACCCG 887

Qy 863 CGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCA 922  
 | || ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 888 CTCCACTCAACGGAGGGGCTTCTGCGAGGGCCAGGCATTCCAGAAGACCGCCTGCACCA 947

Qy 923 CCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTCCGCTGTGGGCTGG 982  
 || | ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 948 CCATCTGCCCAGTCGATGGGGCGTGGACGGAGTGGAGCAAGTGGTCAGCCTGCAGCACTG 1007

Qy 983 ACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGG 1042  
 | || ||||| ||||| ||||| ||||| | || ||||| ||||| ||||| |||||  
 Db 1008 AGTGTGCCCACTGGCGTAGCCGCGAGTGCATGGCGCCCCACCCAGAACGGAGGCCGTG 1067

Qy 1043 AGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTG 1102

Db 1068 ACTGCAGCGGGACGCTGCTCGACTCTAAGAACTGCACAGATGGGCTGTGCATGCAACTGG 1127  
 Qy 1103 CTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGG 1162  
 Db 1128 AGGCCTCAGGGGATGCGGCGCTGTATGCGGGGCTCGTGGTGGCCATCTTCGTGGTCTGTGG 1187  
 Qy 1163 TCCTGCTGCTGCTTGTCTCATCCTCGTTTATTGCCGGAAGAAGGAGGGGGCTGGACTCAG 1222  
 Db 1188 CAATCCTCATGGCGGTGGGGGTGGTGGTGTACCGCCGCAACTGCCGTGACTTCGACACAG 1247  
 Qy 1223 ATGTGGCTGACTCGTCCATT---CTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCA 1279  
 Db 1248 ACATCACTGACTCATCTGCTGCCCTGACTGGTGGTTTCCACCCCGTCAACTTTAAGACGG 1307  
 Qy 1280 GCAAAGCAGACAACCCCCATCTGCT-----CACCATCCAGCCGGACCTCAGCACCACCA 1333  
 Db 1308 CAAGGCCAGTAACCCGCAGCTCCTACACCCCTCTGTGCCTCCTGACCTGACAGCCAGCG 1367  
 Qy 1334 CCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGA----- 1370  
 Db 1368 CCGGCATCTACCGCGGACCCGTGTATGCCCTGCAGGACTCCACCGACAAAATCCCCATGA 1427  
 Qy 1371 -----TGGGCCCAGCCCCAAGTTCCAGCTCACCA----- 1399  
 Db 1428 CCAACTCTCCTCTGCTGGACCCCTTACCCAGCCTTAAGGTCAAGGTCTACAGCTCCAGCA 1487  
 Qy 1400 --ATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACAC-----ACTGCACC 1447  
 Db 1488 CCACGGGCTCTGGGCCAGGCCTGGCAGATGGGGCTGACCTGCTGGGGGTCTTGCCGCCTG 1547  
 Qy 1448 ACAGCTCTCCACCTCTGAGGCCGAGGAGTTCTGCTCTCCGCCTCTCCACCCAGAACTACT 1507  
 Db 1548 GCACATACCTAGCGATTTCGCCCCGGGACACCCACTTCCTGCACCTGCGCAGCGCCAGCC 1607  
 Qy 1508 TCCGCTC-----CCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCT 1552  
 Db 1608 TCGGTTCCCAGCAGCTCTTGGGCCTGCCCCGAGACCCAGGGAGCAGCGTCAGCGGCACCT 1667  
 Qy 1553 TCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCC 1612  
 Db 1668 TTGGCTGCCTGGGTGGGAGGCTCAGCATCCCCGGCACAGGGGTGAGCTTGCTGGTGCCCA 1727  
 Qy 1613 CAGATGCCATACCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAG 1672  
 Db 1728 ATGGAGCCATTCCCCAGGGCAAGTTCTACGAGATGTATCTACTCATCAACAAGGCAGAAA 1787  
 Qy 1673 ACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGAC 1732  
 Db 1788 GTACCCTGCCGCTTTCAGAAGGGACCCAGACAGTATTGAGCCCCTCGGTGACCTGTGGAC 1847  
 Qy 1733 CCCCTGGCGTCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCA 1792  
 Db 1848 CCACAGGCCTCCTGCTGTGCCGCCCCGTCATCCTCACCATGCCCCACTGTGCCGAAGTCA 1907  
 Qy 1793 GCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATG 1852

Db	1908	GTGCCCGTGACTGGATCTTTTCAGCTCAAGACCCAGGCCACCAGGGCCACTGGGAGGAGG	1967
Qy	1853	TGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTG	1912
Db	1968	TGGTGACCTTGGATGAGGAGACCCTGAACACACCCTGCTACTGCCAGCTGGAGCCAGGG	2027
Qy	1913	CCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCG	1972
Db	2028	CCTGTCACATCCTGCTGGACCAGCTGGGCACCTACGTGTTACGGGCGAGTCTATTCCC	2087
Qy	1973	TGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCG	2032
Db	2088	GCTCAGCAGTCAAGCGGCTCCAGCTGGCCGTCTTCGCCCCCGCCCTCTGCACCTCCCTGG	2147
Qy	2033	AGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACCTCAAGGAGGTGGTGC	2092
Db	2148	AGTACAGCCTCCGGGTCTACTGCCTGGAGGACACGCCTGTAGCACTGAAGGAGGTGCTGG	2207
Qy	2093	AGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCTGCACTTCAAGG	2152
Db	2208	AGCTGGAGCGGACTCTGGGCGGATACTTGGTGGAGGAGCCGAAACCGCTAATGTTCAAGG	2267
Qy	2153	ACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGGAAGAGTA	2212
Db	2268	ACAGTTACCACAACCTGCGCCTCTCCCTCCATGACCTCCCCATGCCCATTTGGAGGAGCA	2327
Qy	2213	AGCTCCTTGTGAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGT	2272
Db	2328	AGCTGCTGGCCAAATACCAGGAGATCCCCTTCTATCACATTTGGAGTGGCAGCCAGAAGG	2387
Qy	2273	ACTTGCACTGCACCTTCACCCTGGAGCGTGTGAGCCCAGCACTAGTGACCTGGCCTGCA	2332
Db	2388	CCCTCCACTGCACCTTTCACCCTGGAGAGGCACAGCTTGGCCTCCACAGAGCTCACCTGCA	2447
Qy	2333	AGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCA	2392
Db	2448	AGATCTGCGTGCGGCAAGTGGAAGGGGAGGGCCAGATATTCCAGCTGCATACCACTCTGG	2507
Qy	2393	CCAAG---GACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAG	2449
Db	2508	CAGAGACACCTGCTGGCTCCCTGGACACTCTCTGCTCTGCCCTGGCAGCACTGTACCA	2567
Qy	2450	CCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCTCATTCGGCAGAAGATAATTTCCA	2509
Db	2568	CCCAGCTGGGACCTTATGCCTTCAAGATCCCACTGTCCATCCGCCAGAAGATATGCAACA	2627
Qy	2510	GCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCAGAACTCCACC	2569
Db	2628	GCCTAGATGCCCCCAACTCACGGGGCAATGACTGGCGGATGTTAGCACAGAAGCTCTCTA	2687
Qy	2570	TGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACC	2629
Db	2688	TGGACCGGTACCTGAATTACTTTGCCACCAAAGCGAGCCCCACGGGTGTGATCCTGGACC	2747
Qy	2630	TGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTG	2689
Db	2748	TCTGGGAAGCTCTGCAGCAGGACGATGGGGACCTCAACAGCCTGGCGAGTGCCTTGGAGG	2807



Qy 2690 GACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTGCGGAGGCTGAGTGCTGA 2742  
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 Db 2808 AGATGGGCAAGAGTGAGATGCTGGTGGCTGTGGCCACCGACGGGGACTGCTGA 2860

RESULT 15

US-10-218-779-3

; Sequence 3, Application US/10218779

; Publication No. US20040029222A1

; GENERAL INFORMATION:

; APPLICANT: Edinger, Shlomit

; APPLICANT: MacDougall, John

; APPLICANT: Millet, Isabelle

; APPLICANT: Ellerman, Karen

; APPLICANT: Stone, David

; APPLICANT: Gerlach, Valerie

; APPLICANT: Grosse, William

; APPLICANT: Alsobrook II, John

; APPLICANT: Lepley, Denise

; APPLICANT: Rieger, Daniel

; APPLICANT: Burgess, Catherine

; APPLICANT: Casman, Stacie

; APPLICANT: Spytek, Kimberly

; APPLICANT: Boldog, Ferenc

; APPLICANT: Li, Li

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Mishra, Vishnu

; APPLICANT: Patturajan, Meera

; APPLICANT: Shenoy, Suresh

; APPLICANT: Rastelli, Luca

; APPLICANT: Tchernev, Velizar

; APPLICANT: Vernet, Corine

; APPLICANT: Zerhusen, Bryan

; APPLICANT: Malyankar, Uriel

; APPLICANT: Guo, Xiaojia

; APPLICANT: Miller, Charles

; APPLICANT: Gangolli, Esha

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-214

; CURRENT APPLICATION NUMBER: US/10/218,779

; CURRENT FILING DATE: 2002-08-14

; PRIOR APPLICATION NUMBER: 60/253,834

; PRIOR FILING DATE: 2000-11-29

; PRIOR APPLICATION NUMBER: 60/250,-926

; PRIOR FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: 60/264,180

; PRIOR FILING DATE: 2001-01-25

; PRIOR APPLICATION NUMBER: 60/313,656

; PRIOR FILING DATE: 2001-08-20

; PRIOR APPLICATION NUMBER: 60/327,456

; PRIOR FILING DATE: 2001-10-05

; NUMBER OF SEQ ID NOS: 216

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 2860

; TYPE: DNA

; ORGANISM: Homo sapiens  
US-10-218-779-3

Query Match 34.0%; Score 936.2; DB 13; Length 2860;  
Best Local Similarity 61.7%; Pred. No. 9e-228;  
Matches 1662; Conservative 0; Mismatches 938; Indels 93; Gaps 7;

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Qy      143 ACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATG 202
      || | | | || | | | | | | | | | | | | | | | | | | |
Db      168 ACTCCTTCCCCGTCAGCGCCAGCAGAGCCGCTGCCCTACTTCCTGCAGGAGCCACAGGACG 227

Qy      203 TGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGCAAGGCCGTGCCCCGCCACGCAGA 262
      || || | | | | | | | | | | | | | | | | | | | | | |
Db      228 CCTACATTGTGAAGAACAAGCCTGTGGAGCTTCGCTGCCGCGCCTTCCCCGCCACACAGA 287

Qy      263 TCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCA 322
      || | | | | | | | | | | | | | | | | | | | | | | |
Db      288 TCTACTTCAAGTGCAACGGCGAGTGGGTGAGCCAGAACGACCACGTACACAGGAAGGCC 347

Qy      323 CAGACGGGAGCAGTGGGCTGCCCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGG 382
      || | | | | | | | | | | | | | | | | | | | | | | |
Db      348 TGGATGAGGCCACCGGCCCTGCGGGTGCGCGAGGTGCAGATCGAGGTGTCGCGGCAGCAGG 407

Qy      383 TCGAGAAGGTGTTTCGGGCTGGAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGG 442
      | | | | | | | | | | | | | | | | | | | | | | | | |
Db      408 TGGAGGAGCTCTTTGGGCTGGAGGATTACTGGTGCCAGTGCGTGGCCTGGAGCTCCGCAG 467

Qy      443 GCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGC 502
      || | | | | | | | | | | | | | | | | | | | | | | |
Db      468 GCACCACCAAGAGTCGCGCGAGCCTACGTCCGCATCGCCTACCTGCGCAAGAACTTCGATC 527

Qy      503 AGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCAC 562
      || | | | | | | | | | | | | | | | | | | | | | | |
Db      528 AGGAGCCTCTGGGCAAGGAGGTGCCCCTGGACCATGAGGTTCTCCTGCAGTGCCGCCCGC 587

Qy      563 CGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGT 622
      || | | | | | | | | | | | | | | | | | | | | | | |
Db      588 CGGAGGGGGTGCCTGTGGCCGAGGTGGAATGGCTCAAGAATGAGGATGTCATCGACCCCA 647

Qy      623 CCCTGGACCCCAATGTATACATCACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCC 682
      || | | | | | | | | | | | | | | | | | | | | | | |
Db      648 CCCAGGACACCAACTTCCTGCTCACCATCGACCACAACCTCATCATCCGCCAGGCCCGCC 707

Qy      683 TTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAACATCGTGGCACGTGCGCCGAGCG 742
      | | | | | | | | | | | | | | | | | | | | | | | | |
Db      708 TGTCGGACACTGCCAACTATACCTGCGTGGCCAAGAACATCGTGGCCAAACGCCGGAGCA 767

Qy      743 CCTCCGCTGCTGTGTCATCGTCTACGTGAACGGTGGGTGGTCGACGTGGACCGAGTGGTCCG 802
      || | | | | | | | | | | | | | | | | | | | | | | |
Db      768 CCACTGCCACCGTCATCGTCTACGTGAATGGCGGCTGGTCCAGCTGGGCAGAGTGGTCAC 827

Qy      803 TCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGG 862
      || | | | | | | | | | | | | | | | | | | | | | | |
Db      828 CCTGCTCCAACCGCTGTGGCCGAGGCTGGCAGAAGCGCACCCGGACCTGCACCAACCCCG 887

Qy      863 CGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCA 922
      | | | | | | | | | | | | | | | | | | | | | | | | |
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Db	888	CTCCACTCAACGGAGGGGCTTCTGCGAGGGCCAGGCATTCCAGAAGACCGCCTGCACCA	947
Qy	923	CCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGG	982
Db	948	CCATCTGCCCAGTCGATGGGGCGTGGACGGAGTGGAGCAAGTGGTCAGCCTGCAGCACTG	1007
Qy	983	ACTGCACCCACTGGCGGAGCCGTGAGTGTCTGTACCCAGCACCCCGCAACGGAGGGGAGG	1042
Db	1008	AGTGTGCCCCTACTGGCGTAGCCGCGAGTGCATGGCGCCCCCACCCAGAACGGAGGCCGTG	1067
Qy	1043	AGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTG	1102
Db	1068	ACTGCAGCGGGACGCTGCTCGACTCTAAGAACTGCACAGATGGGCTGTGCATGCAACTGG	1127
Qy	1103	CTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGG	1162
Db	1128	AGGCCTCAGGGGATGCGGCGCTGTATGCGGGGCTCGTGGTGGCCATCTTCGTGGTTCGTGG	1187
Qy	1163	TCCTGCTGCTGCTTGTCTCTCATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAG	1222
Db	1188	CAATCCTCATGGCGGTGGGGGTGGTGGTGTACCGCCGCAACTGCCGTGACTTCGACACAG	1247
Qy	1223	ATGTGGCTGACTCGTCCATT---CTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCA	1279
Db	1248	ACATCACTGACTCATCTGCTGCCCTGACTGGTGGTTTCCACCCCGTCAACTTTAAGACGG	1307
Qy	1280	GCAAAGCAGACAACCCCCATCTGCT-----CACCATCCAGCCGGACCTCAGCACCACCA	1333
Db	1308	CAAGGCCCAGTAACCCGCAGCTCCTACACCCCTCTGTGCCTCCTGACCTGACAGCCAGCG	1367
Qy	1334	CCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGA-----	1370
Db	1368	CCGGCATCTACCGCGGACCCGTGTATGCCCTGCAGGACTCCACCGACAAAATCCCCATGA	1427
Qy	1371	-----TGGGCCAGCCCCAAGTTCCAGCTCACCA-----	1399
Db	1428	CCAACTCTCCTCTGCTGGACCCCTTACCCAGCCTTAAGGTCAAGGTCTACAGCTCCAGCA	1487
Qy	1400	--ATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACAC-----ACTGCACC	1447
Db	1488	CCACGGGCTCTGGGCCAGGCCCTGGCAGATGGGGCTGACCTGCTGGGGGTCTTGCCGCCTG	1547
Qy	1448	ACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAGAATACTACT	1507
Db	1548	GCACATAACCCTAGCGATTTGCCCCGGGACACCCACTTCTGCACCTGCGCAGCGCCAGCC	1607
Qy	1508	TCCGCTC-----CCTGCCCGGAGGCACCAGCAACATGACCTATGGGACCT	1552
Db	1608	TCGGTTCCAGCAGCTCTTGGGCCTGCCCCGAGACCCAGGGAGCAGCGTCAGCGGCACCT	1667
Qy	1553	TCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCC	1612
Db	1668	TTGGCTGCCTGGGTGGGAGGCTCAGCATCCCCGGCACAGGGGTGAGCTTGCTGGTGCCCA	1727
Qy	1613	CAGATGCCATAACCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAG	1672
Db	1728	ATGGAGCCATTCCCCAGGGCAAGTTCTACGAGATGTATCTACTCATCAACAAGGCAGAAA	1787

Qy	1673	ACGTGAGGTTGCCCTAGCTGGCTGTCAGACCCCTGCTGAGTCCCATCGTTAGCTGTGGAC	1732
Db	1788	GTACCCTGCCGCTTTTCAGAAGGGACCCAGACAGTATTGAGCCCCTCGGTGACCTGTGGAC	1847
Qy	1733	CCCCTGGCGTCTCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCA	1792
Db	1848	CCACAGGCCTCCTGCTGTGCCGCCCGTCATCCTCACCATGCCCACTGTGCCGAAGTCA	1907
Qy	1793	GCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGGAGCTGGGAGGATG	1852
Db	1908	GTGCCCCTGACTGGATCTTTTCAGCTCAAGACCCAGGCCACCAGGGCCACTGGGAGGAGG	1967
Qy	1853	TGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGTG	1912
Db	1968	TGGTGACCCTGGATGAGGAGACCCTGAACACACCCTGCTACTGCCAGCTGGAGCCCAGGG	2027
Qy	1913	CCTGCTACGTCTTCACCGAGCAGCTGGGCGCCTTTGCCCTGGTGGGAGAGGCCCTCAGCG	1972
Db	2028	CCTGTACATCCTGCTGGACCAGCTGGGCACCTACGTGTTACAGGGCGAGTCCTATTCCC	2087
Qy	1973	TGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCG	2032
Db	2088	GCTCAGCAGTCAAGCGGCTCCAGCTGGCCGTCTTCGCCCCCGCCCTCTGCACCTCCCTGG	2147
Qy	2033	AGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGC	2092
Db	2148	AGTACAGCCTCCGGGTCTACTGCCTGGAGGACACGCCTGTAGCACTGAAGGAGGTGCTGG	2207
Qy	2093	AGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGG	2152
Db	2208	AGCTGGAGCGGACTCTGGGCGGATACTTGGTGGAGGAGCCGAAACCGCTAATGTTCAAGG	2267
Qy	2153	ACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGGAAGAGTA	2212
Db	2268	ACAGTTACCACAACCTGCGCCTTCCCTCCATGACCTCCCCCATGCCATTGGAGGAGCA	2327
Qy	2213	AGCTCCTTGTGCTAGCTACCAGGAGATCCCCCTTTTATCACATCTGGAATGGCACGCAGCGGT	2272
Db	2328	AGCTGCTGGCCAAATACCAGGAGATCCCCCTTCTATCACATTTGGAGTGGCAGCCAGAAGG	2387
Qy	2273	ACTTGCACTGCACCTTCACCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCA	2332
Db	2388	CCCTCCACTGCACCTTCACCTGGAGAGGCACAGCTTGGCCTCCACAGAGCTCACCTGCA	2447
Qy	2333	AGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCA	2392
Db	2448	AGATCTGCGTGCGGCAAGTGGAGGGGAGGGCCAGATATTCCAGCTGCATACCACTCTGG	2507
Qy	2393	CCAAG---GACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAG	2449
Db	2508	CAGAGACACCTGCTGGCTCCCTGGACACTCTCTGCTCTGCCCCCTGGCAGCACTGTCACCA	2567
Qy	2450	CCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCCTTCCTCATTCGGCAGAAGATAATTTCCA	2509
Db	2568	CCCAGCTGGGACCTTATGCCTTCAAGATCCCCTGTCCATCCGCCAGAAGATATGCAACA	2627

